

## Protein Sequence Searches - February 2005

All of the sequence databases on ARSS have recently been updated.



- **Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt.** These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rnp**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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Range: from  to 
 Features:
 ☐ SNP
 ☐ CDD
 ☒ MGC
 ☐ HPRD
 ☐ STS

☐ 1: [CAC07879](#). Reports unnamed protein p...[gi:10046113]

[BLink](#), [Links](#)

LOCUS CAC07879 417 aa linear UNA 24-NOV-2000  
 DEFINITION unnamed protein product [unidentified].  
 ACCESSION CAC07879  
 VERSION CAC07879.1 GI:10046113  
 DBSOURCE embl accession [AX022514.1](#)  
 KEYWORDS .  
 SOURCE unidentified  
 ORGANISM [unidentified](#)  
 unclassified.  
 REFERENCE 1  
 AUTHORS Flegel,W.A. and Wagner,F.F.  
 TITLE Novel nucleic acid molecules correlated with the rhesus weak d phenotype  
 JOURNAL Patent: WO 9937763-A 29-JUL-1999;  
 FLEGEL WILLY A (DE) ; WAGNER FRANZ F (DE) ; DRK BLUTSPENDEDIENST BADEN WUE (DE)  
 FEATURES Location/Qualifiers  
 source 1..417  
 /organism="unidentified"  
 /db\_xref="taxon:32644"  
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 /name="unnamed protein product"  
[CDS](#) 1..417  
 /coded\_by="AX022514.1:1..1254"

#### ORIGIN

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1 msskyprsvr rclplwaltl eaalillfyf fthydasled qkglvasyqv gqdltvmaai
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121 lsvlisvdav lgkvnlaqlv vmvlvevtal gnrmvisni fntdyhmnm hiyvfaayfg
181 lsvawclpkp lpegtdkdq tatipslsam lgalflwmfw psfnsallrs pierknafn
241 tyyavavsvv taisgsslah pggkisktyv hsavlaggva vgtschlips pwlamvlgv
301 aglisvggak ylpgccnrvl giphssimgy nfsllgllge iiyivllvld tvgagnmig
361 fqvllsigel slaivialts glltglllnl kiwkapheak yfddqvfwkf phlavgf

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Feb 9 2005 14:31:10

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 24, 2005, 13:13:49 ; Search time 24 Seconds  
(without alignments)  
1297.027 Million cell updates/sec

Title: CAC07879

Perfect score: 2124

Sequence: 1 MSCKYRSVRGRLPLCALTL.....EAKYFDQVFWKPHLAVGF 417

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing filter 45 summaries

Database :  
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3: /cgnt2\_6/prodata/1/1aa/6A COMB .pep.\*  
4: /cgnt2\_6/prodata/1/1aa/6B COMB .pep.\*  
5: /cgnt2\_6/prodata/1/1aa/6C COMB .pep.\*  
6: /cgnt2\_6/prodata/1/1aa/6D COMB .pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1833	86.3	417	1 US-08-553-888A-3	Sequence 3, Appl1
2	552.5	26.0	418	4 US-09-949-016-7328	Sequence 7328, Ap
3	497	23.4	487	4 US-09-949-016-9649	Sequence 9649, Ap
4	202	9.5	145	4 US-09-461-325-438	Sequence 438, App
5	202	9.5	145	4 US-10-012-542-438	Sequence 438, App
6	202	9.5	145	4 US-10-115-123-438	Sequence 438, App
7	142	6.7	308	4 US-09-461-325-437	Sequence 437, App
8	142	6.7	308	4 US-10-012-542-437	Sequence 437, App
9	142	6.7	308	4 US-10-115-123-437	Sequence 437, App
10	117.5	5.6	633	4 US-09-248-766A-20407	Sequence 20407, A
11	114	5.4	801	4 US-09-710-379-2020	Sequence 2020, Ap
12	114	5.4	808	4 US-09-134-001C-3105	Sequence 3105, Ap
13	113.5	5.3	447	4 US-09-489-039A-7527	Sequence 7527, Ap
14	110	5.2	800	4 US-09-134-001C-5655	Sequence 5655, Ap
15	109.5	5.2	407	4 US-09-489-039A-10855	Sequence 10855, A
16	109.5	5.2	464	4 US-09-252-991A-18525	Sequence 18525, A
17	109	5.1	449	4 US-09-543-681A-6546	Sequence 6546, Ap
18	108.5	5.1	447	4 US-10-162-012-29	Sequence 29, Appl
19	108.5	5.1	509	4 US-09-252-991A-30864	Sequence 30864, A
20	108.5	5.1	518	4 US-09-252-991A-31586	Sequence 31586, A
21	107	5.0	443	4 US-09-328-352-6978	Sequence 6978, Ap
22	107	5.0	447	4 US-09-489-039A-11893	Sequence 11893, A
23	107	5.0	448	4 US-09-583-110-4040	Sequence 4040, Ap
24	107	5.0	452	4 US-09-107-433-5105	Sequence 5105, Ap
25	106.5	5.0	478	4 US-09-328-352-7771	Sequence 7771, Ap
26	106.5	5.0	517	4 US-09-252-991A-19322	Sequence 19322, A
27	104.5	4.9	437	3 US-09-134-001C-4808	Sequence 4808, Ap

28	104	4.9	401	4 US-09-328-352-5448	Sequence 5448, Ap
29	104	4.9	465	4 US-09-603-208A-258	Sequence 258, App
30	103	4.8	484	4 US-09-252-991A-30013	Sequence 30013, A
31	103	4.8	484	4 US-09-489-039A-11054	Sequence 11054, A
32	101.5	4.8	483	4 US-09-107-532A-4123	Sequence 4123, App
33	101	4.8	181	4 US-09-461-325-196	Sequence 196, App
34	101	4.8	181	4 US-10-012-542-196	Sequence 196, App
35	101	4.8	181	4 US-10-115-123-196	Sequence 196, App
36	101	4.8	448	4 US-09-543-681A-7245	Sequence 7245, Ap
37	101	4.8	470	4 US-09-489-039A-8514	Sequence 8514, Ap
38	101	4.8	511	4 US-09-543-681A-7476	Sequence 7476, Ap
39	100.5	4.7	486	4 US-10-033-109-12	Sequence 12, Appl
40	100.5	4.7	1323	4 US-09-270-767-46728	Sequence 46728, A
41	100	4.7	418	4 US-09-489-039A-12883	Sequence 12883, A
42	100	4.7	437	4 US-09-830-433A-12	Sequence 12, Appl
43	100	4.7	548	4 US-09-328-352-6605	Sequence 6605, Ap
44	100	4.7	565	4 US-09-602-787A-616	Sequence 616, App
45	99.5	4.7	1607	4 US-09-902-540-16765	Sequence 16765, A

# ALIGNMENTS

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RESULT 1
US-08-553-888A-3
; Sequence 3, Application US/08553888A
; Patent No. 5723293
; GENERAL INFORMATION:
; APPLICANT: Huang
; TITLE OF INVENTION: DIAGNOSTIC METHOD AND KIT FOR
; TITLE OF INVENTION: DETERMINING RH BLOOD GROUP GENOTYPE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann & Baron, LLP
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: USA
; ZIP: 11753
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553, 888A
; FILING DATE: 11/06/95
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: O'Dea, Sean W.
; REGISTRATION NUMBER: 37690
; REFERENCE/DOCKET NUMBER: 454-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-553-888A-3

Query Match      86.3%; Score 1833; DB 1; Length 417;
Best Local Similarity 88.7%; Pred. No. 4, 6e-184;
Matches 370; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

QY      1 MSCKYRSVRGRLPLCALTLLEFPTHYDASLEQKGVASVYGVODLTWAAI 60
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Db      1 MSCKYRSVRGRLPLCALTLLEFPTHYDASLEQKGVASVYGVODLTWAAI 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      61 GIGFLTSSFRHSSVAFFNLFWALGVQVAILLDGFLSQPSGKVVITLFSIWLATMSA 120
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Db      61 GIGFLTSNFRHSSWSSVAFNLFWALGVOMAILLDFLSQPPGKVITLFSIRLATMSA 120
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Db      121 MSVLTSAGAVLGVNLAOLVWVTVLVEVTDGLNLRWVTSINIENTVDHMMNHIVYPAAYFG 180
Qy      181 LTVAMCLPKPLPEGTEDNDQORATIPSLSAMLGALFLMMPRPVSNSALLRSPERKNAAVEN 240
Db      181 LTVAMCLPKPLPEGTEDNDQORATIPSLSAMLGALFLMMPRPVSNSALLRSPERKNAAVEN 240
Qy      241 TYVAAVSVVTAISSGSLAHPOGKISKYTGHSAYLPEGVAVDTSCHLIPSPWLPVILGV 300
Db      241 TYVAAVSVVTAISSGSLAHPOGKISKYTGHSAYLPEGVAVDTSCHLIPSPWLPVILGV 300
Qy      301 AGLISVGAAYLPGCCNRYLGIPIHSSINGVNSLLGLEELIYIYLVLDVTVGANGMIG 360
Db      301 AGLISVGAAYLPGCCNRYLGIPIHSSINGVNSLLGLEELIYIYLVLDVTVGANGMIG 360
Qy      361 FOVLISIGELSLAIYIALTSGLTALLNLKIRKAPHEAKYFDDQVFWKPHLAVGF 417
Db      361 FOVLISIGELSLAIYIALTSGLTALLNLKIRKAPHEAKYFDDQVFWKPHLAVGF 417

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## RESULT 2

```

US-09-949-016-7328
; Sequence 7328, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7328
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7328

```

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Query Match      26.0%; Score 552.5; DB 4; Length 418;
Best Local Similarity 34.1%; Pred. No. 2.4e-49;
Matches 140; Conservative 78; Mismatches 171; Indels 21; Gaps 7;

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```

Qy      14 PLCAITLLEALLILFFFTYH--DASLEDQKGLVASYVG-----ODLTVMALIGL 62
Db      15 PLMAIVLEIMIVLFGFVEYETDQVLEQINTKPTDWCIFPELYPLFDVHVMIFVGF 74
Qy      63 GFLTSSFRHSSWSSVAFNLFWALGVOMAILLDFLSQPPGKVITLFSIRLATMSA 122
Db      75 GFLMTFLKTKGFSVGNLNLVLAALGQWGTIVGIL--QSQGQKFNIGIKMIMADPSAAT 133
Qy      123 VLISVDVAIVGVNLAOLVWVTVLVEVTDGLNLRWVTSINIENTVDHMMNHIVYPAAYFG 182
Db      134 VLISFGAVIGKTSPTQWLIMTIEIVFPAINEYLVSEIFASDIGASMTIHAFGAYFG 193
Qy      183 VAMCLPKPLPEGTEDNDQORATIPSLSAMLGALFLMMPRPVSNSALLRSPERKNAAVEN 242
Db      194 VAGILVRSGLRKHNEBESAYVSDLFAMIGTFLFMFMFSPNSALIPGDKOCRAIVNY 253
Qy      243 YAAVAVSVVTAISSGSLAHPOGKISKYTGHSAYLPEGVAVDTSCHLIPSPWLPVILGV 302
Db      254 FSLAACVTLFAFASLSVHERGKLMNVHIOVATLAGGVAAGTCAADMAIHFGMIGISIA 313
Qy      303 LISVRGAKYLPGCCNRYLGIPIHSSINGVNSLLGLEELIYIYLVLDVTVGANGMIG 361

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Db      314 MSVLGYKFLPLPFTTKRI-HDTGCVNHLHJPGVGVGAGIYAAVM--GASNTSMAM 369
Qy      362 QVLISIGELSLAIYIALTSGLTALLNLKIRKAPHEAKYFDDQVFWKPHLAVGF 417
Db      370 QA-----AALSSIGTAVVGSGLMTGLIKLPLMQQPSDQNCYDSDVYWKQF 415

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## RESULT 3

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US-09-949-016-9649
; Sequence 9649, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9649
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9649

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Query Match      23.4%; Score 497; DB 4; Length 487;
Best Local Similarity 29.4%; Pred. No. 2.1e-43;
Matches 129; Conservative 77; Mismatches 183; Indels 50; Gaps 8;

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Qy      13 LPLCAITLLEALLILFFFTYH-----ASLEDQKGLVASYVGODLTVMALIGL 58
Db      19 LPLTCLLQVIMVILFGFVAYDPEADAHMWSERTKQLSDMNEFFRYRPSFDVHVMV 78
Qy      59 AIGLFLTSSFRHSSWSSVAFNLFWALGVOMAILLDFLSQPPGKVITLFSIRLATMSA 118
Db      79 FVGFGLMTFLQRYGFSAYGVNFLLAAGIQWMTLQWMPHFLQDRYIVGVEVNLINDF 138
Qy      119 SALSVLSDVAIVGVNLAOLVWVTVLVEVTDGLNLRWVTSINIENTVDHMMNHIVYPAAY 178
Db      139 CVASVCVAFGAVLGVSPIDQLIMTFPQVTLFAVNEFLIMLKYKAGSGMTIHTFGAY 198
Qy      179 FGLTVAMCLPKPLPEGTEDNDQORATIPSLSAMLGALFLMMPRPVSNSALLRSPERKNAAV 238
Db      199 FGLTVTRILYRNLNEQSKERQNSVYQSDLFAMIGTFLFMFMFSPNSALISHTGSCRRAA 258
Qy      239 FRTYAAVAVSVVTAISSGSLAHPOGKISKYTGHSAYLPEGVAVDTSCHLIPSPWLPVILG 298
Db      259 INTYCSLAAVLTVAISSALHKKGKLDWVHIOVATLAGGVAAGTAAEMMLMPYCALIIG 318
Qy      299 LVAGLISVGAAYL-----PGCC--NRVIGIPIHSSINGVNSLLGLEELIYIYLV 346
Db      319 FVCGIISTLGLVLPFLERLHIQDTGGINNHGIP-----GIGIGVAGAVTAAS 369
Qy      347 LVLDTVGANGMT-----GF-----QVLISIGELSLAIYIALTSGLTALLNLK 392
Db      370 ASLEVYVGK-EGLVASDFPGFNGDWTARTQOKPQIYGLVLTLMALMAGIIVGILRLPF 428
Qy      393 RKAPHEAKYFDDQVFWKPHLAVGF 417
Db      429 WQPSDQNCYDSDVYWKQF 415

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```

RESULT 4
US-09-461-325-438
; Sequence 438, Application US/09461325A

```

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? Patent No.6475753
? GENERAL INFORMATION:
? APPLICANT: Ruben et al.
? TITLE OF INVENTION: 94 Human Secreted Proteins
? FILE REFERENCE: P2029P1
? CURRENT APPLICATION NUMBER: US/09/461,325A
? EARLIER FILING DATE: 1999-12-14
? EARLIER APPLICATION NUMBER: PCT/US99/13418
? EARLIER FILING DATE: 1999-06-15
? EARLIER APPLICATION NUMBER: 60/089,507
? EARLIER FILING DATE: 1998-06-16
? EARLIER APPLICATION NUMBER: 60/089,508
? EARLIER FILING DATE: 1998-06-16
? EARLIER APPLICATION NUMBER: 60/089,509
? EARLIER FILING DATE: 1998-06-16
? EARLIER APPLICATION NUMBER: 60/089,510
? EARLIER FILING DATE: 1998-06-16
? EARLIER APPLICATION NUMBER: 60/090,112
? EARLIER FILING DATE: 1998-06-22
? EARLIER APPLICATION NUMBER: 60/090,113
? EARLIER FILING DATE: 1998-06-22
? NUMBER OF SEQ ID NOS: 532
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 438
? LENGTH: 145
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-461-325-438

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Query Match Similarity      9.5%: Score 202; DB 4; Length 145;
Best Local Similarity      34.3%: Pred. No. 3, 7e-13;
Matches 49; Conservative 24; Mismatches 70; Indels 0; Gaps 0

QY      142 MVLVEVTDLGNLRVVISNIPTDYHMMNMHHIVYFAAYFGLTVAWCLPKPELPEGTEDNDOR 201
Dh      1 MTFPEQVTLFAVAVEFILLILMLLKVDAGCSMTIHTFGAYFGLTVTRILYLRNNEQSGERQNS 60
QY      202 ATIPSLAMGLALPLMPRPSPNSALLSPIERKNAVFNVTYAAVAVSVYATLSSGLAHP 261
Dh      61 VYQSDLPFMMIGLFLFMMTPSPNSAISYHGDSQHRPAINTVCSLAVALTVSAISSALHK 120
QY      262 QGKISKTYGHSAGVLEPGVAVDTS 284
Dh      121 KGKLDVHIIQNTATLAGVAVGTA 143

RESULT 5
US-10-012-542-438
; Sequence 438, Application US/10012542
; Patent No. 6627741
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P202991
; CURRENT APPLICATION NUMBER: US/10/012,542
; PRIOR APPLICATION NUMBER: 2001-12-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,355
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 438

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[illegible][illegible]

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: Sequence 437, Application US/09461325A
: Patent No. 6475753
:
: GENERAL INFORMATION:
: APPLICANT: Ruben et al.
: TITLE OF INVENTION: 94 Human Secreted Proteins
: FILE REFERENCE: P2029P1
: CURRENT APPLICATION NUMBER: US/09/461,325A
: CURRENT FILING DATE: 1999-12-14
: EARLIER APPLICATION NUMBER: PCT/US99/13418
: EARLIER FILING DATE: 1999-06-15
: EARLIER APPLICATION NUMBER: 60/089,507
: EARLIER FILING DATE: 1998-06-16
: EARLIER APPLICATION NUMBER: 60/089,508
: EARLIER FILING DATE: 1998-06-16
: EARLIER APPLICATION NUMBER: 60/089,509
: EARLIER FILING DATE: 1998-06-16
: EARLIER APPLICATION NUMBER: 60/089,510
: EARLIER FILING DATE: 1998-06-16
: EARLIER APPLICATION NUMBER: 60/090,112
: EARLIER FILING DATE: 1998-06-22
: EARLIER APPLICATION NUMBER: 60/090,113
: EARLIER FILING DATE: 1998-06-22
: NUMBER OF SEQ ID NOS: 532
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 437
: LENGTH: 308
: TYPE: PRT
:
: ORGANISM: Homo sapiens
: US-09-461-325-437

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Query Match      6.7%; Score 142; DB 4; Length 308;
Best Local Similarity 25.0%; Pred. No. 2.4e-06;
Matches 47; Conservative 32; Mismatches 71; Indels 38; Gaps 7

QY      252 AIGSSSLAHP--QGKISKTYGHSALTPGVAVDTSCHLIPSEFWLTVLGLVAGLISYVGA 309
      91 AYLGNIGQCPAKKGLDMVHTIONATLAGVAVGTAAEMLMYPGALLIGFVGIISTIGF 150
QY      310 KYL-----PQCC--NRVLGIPHSINGYNFSLGLLEETIYYLLVLDITYGAGNG 357
      151 VYLLPFLESRLHIDTQCGINNLAHGIP-----GIIGGVAGVATAASASLEVVGK-EG 200
QY      358 MI-----GF-----QVLLSTGELSLATVIALTSGTLTALLNLRKAPKHEAKYFD 403
      201 LVHSFDPGFGFNGDMTARTQGRFQIYGLVLTVALMALMGIIYGLIURLPFWGQSPDENCEPE 260
Db
QY      404 DOVEFKFP 411
      261 DAVYVEMP 268

RESULT 8
US-10-012-542-437
/ Sequence 437, Application US/10012542
/ Patent No. 6627741
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: 94 Human Secreted Proteins
/ FILE REFERENCE: P2029p1
/ CURRENT APPLICATION NUMBER: US/10/012,542
/ PRIOR FILING DATE: 2001-12-12
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
/ PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
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/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22

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: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
:
: PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
:
: NUMBER OF SEQ ID NOS: 532
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 437
:
: LENGTH: 308
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens
:
: US-10-012-542-437

```

Query Match	6.7%;	Score 142;	DB 4;	Length 308;
Best Local Similarity	25.0%;	Pred. No. 2.4e-06;		
Matches 47;	Conservative 32;	Mismatches 71;	Indels 38;	Gaps 7;

```

QY      252  A L S G S S L A H P -- Q G K I S T Y G H S A N L P E G V A V D T S C H L I D S P M L P Y I V L G V A G I I S V R G A 309
Db      91  A Y I G G N I Q C P A K K G L D M V H I O N K L A G V A V G T R A E M L M P Y G A L I G V C G I I S T L G F 150

QY      310  K Y L ----- P G C C -- N R V L G I P H S I G M V N P S L L G L B E I I Y V L L V L D T V A G N G 357
Db      151  V Y I T P P L E S R L H I O P T C G I N N L H G P ----- G I G G I V A V A N T A S A S L E V Y K - E S 200

QY      358  M I ----- G F ----- Q V L I S T G E L S L A I V A L T S G L L T A L L I N K I R A P D H E A K Y P D 403
Db      201  L V H S F D Q F G N D M T A R T Q G K F Q I Y G L L V T L A M L M G G I I V G L I R L P F W G S D E N C E E 260

QY      404  D O Y F W K E P 411
Db      261  D A V Y M E M P 268

```

```

RESULT 9
US-10-115-123-437
; Sequence 437, Application US/10115123
; Patent No. 6774216
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P202930APD2
; CURRENT APPLICATION NUMBER: US/10/115,123
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Patencin Ver. 2.0
; SEQ ID NO 437
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-115-123-437

```

	Query Match	6.7%;	Score 142;	DB 4;	Length 308;	
	Best Local Similarity	25.0%;	Pred. No. 2,4e-06;			
	Matches	47/;	Conservative 32/;	Mismatches 71/;	Indels 38/;	Gaps 7/;
Oy	252 AIGSSSLAHP--GQKTSKTGVSAVLPEGAVDTPSCHLIPSPMLPYLVGLAGLSYRGA	309				
	: : : : :   : : : : :   : : : : :					
Dd	91 AYIGNIGCPAAKKGLDMVHIQNATLAGSVAVGTAAMMLMPFALLIIGFYCGSIITLGF	150				
	: : : : :   : : : : :   : : : : :					
Oy	310 KYL-----PGCC--NRVLGIPIHSSIMGYNFFSLGLLEBIIIVTLVLDTVPVGANG	357				
	: : : : :   : : : : :   : : : : :					



```
Db      151 VYLTPLESRLHIDTGCINNLSGIP-----GIIGIVGAVTAASALEVYCK-EG 200
Qy      358 MI-----GF-----OVLISIGELSLAIVIALTSGLLTALLLNKIRAPHEAYKD 403
Db      201 LVHSFDFQGNRGDWTARTQKRFQYIGLLVTLTLMALMGIIYGLTLRLPFGQSPDENCEFE 260
Qy      404 DOVFWKFP 411
Db      261 DAVYMEMP 268

RESULT 10
US-09-248-796A-20407
; Sequence 20407, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20407
; LENGTH: 633
; TYPE: PR1
; ORGANISM: Candida albicans
US-09-248-796A-20407

Query Match      5.5%; Score 117.5; DB 4; Length 633;
Best Local Similarity 22.1%; Pred. No. 0.0027;
Matches 92; Conservative 69; Mismatches 142; Indels 113; Gaps 22;

Qy      5 YPSVORCLPLCALTEALILLFYFTHYDASLEDDKGLVASYQVGODLTVMAGLGF 64
Db      83 YLHGVC--LILCLSL--FLCLFLFAL-----DQTIYV-----TILTVTKRF 121
Qy      65 LTSSFRHSHSVSAFNLFM-----LALGVOMAILDLGFLSQFSGKVITLF-- 111
Db      122 --DAFSKVGWLSGFLTMAVFIOFGKLSIIIGKKAMV-----IAILFEA 167
Qy      112 -SIWLAETMSLSVLIS--VDAAVGLKNAQLQVVMVAVLEVDLGNLRVNTSINFTDYM- 167
Db      168 GSLMCAIANDMNVYLIGRVLAGIGSGINSLVFVIGSEVVPITRRPLALS-IFSITPVA 226
Qy      168 NMHHIYVFAAYFG-LTVAMCLPKPLPEGTEDNDQRATIPSLAMLGALFLMPPRSVNSA 226
Db      227 SVVGPLIGGAFSTKVTYRMAFYINLPFG-----GPAITVFLYAFPPRPKV 272
Qy      227 LRSPIERKNAVNTYVAVAVSVTALISGSLAHPOCKISKTYGHSVAVLEGVAVDTSC 286
Db      273 NVKQQLKQFD-YFGTPLLIGSVILL-----LAITGTSID-PPMDSAAYVISC- 317
Qy      287 LITSPMLPIYLG--LVAGLSIVGAKYTLRECCNRVLGIPHSISMGNFSLGLLEETIY 343
Db      318 -----FVLGPLYLLIAFVVMNGFSKNQVISTEIVKP--QIIASTLAISGIFSAPIM 367
Qy      344 IYLLVLDTVGAGNMIGFOYL-----LSIGELSLAIVIALTSGLLTALLNLKIRK 394
Db      368 FMIV-----GATFOYVKASPLSAGLHLPTIIAV---VLSMGLSLVOK 411

RESULT 11
US-09-710-279-2020
; Sequence 2020, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
```

```
; FILE REFERENCE: PUJ3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2020
; LENGTH: 801
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-2020

Query Match      5.4%; Score 114; DB 4; Length 801;
Best Local Similarity 20.9%; Pred. No. 0.009;
Matches 103; Conservative 79; Mismatches 172; Indels 138; Gaps 23;

Qy      9 VORCLPLCA-----LTLEALILLFYFTHYDASL-----EDCKGLVASYQVGODLT 55
Db      259 IARTPIFAISEGKWTTTL-VGLITLFW-----ASLNAIKQDHLGILAFSTVSQLCM 311
Qy      56 VMAAIGL-----GFLTSSFRHSHSVSAFNLFMALGVOMAI----- 92
Db      312 IMSWLGIGAVSYHQGANSQLYVAGFVAALFHLINHAIFKALFMITGIDHSGTRDVK 371
Qy      93 LLDGFLSQFSGKVITLFSIWLATMSALSVDVAVL-GKVNAQLQVVMVAVLEVDLG 151
Db      372 KLGGELTIMPISFTLVITTLTSMAGVPPFNGFLSKERFLSMMIVTTLNLSLNTLGLLL 431
Qy      152 NLRNVISNIENTDYHNM-NMHHIYVFAAYFGLTVMCLPKPLPEGTEDNDQRATIPSLAM 210
Db      432 PIAIIGSITFYYSIKFIHLIF-FGSY-----KPAIPKADHSSILMLISPIILT 482
Qy      211 LGALFLMPPRSVNSALLRSPIERKN-----AVFTYVA-----VSU 249
Db      483 SLIVIRGLF-PSI---LTQSLIEPASVAVSQTSNITAEFHLPHDITAPLSTIGIYIIGI 538
Qy      250 VTAISGS-----SLAH-OGKISKTYGHSVAVLEGVAVDTSCILIPS----- 290
Db      539 LLISFSYWRLLQAHFYQLTLNHWY-----DTSGQRIPGYSSENTNSVYTG 586
Qy      291 --PWLPIVLGLVAGLISVRKAKYLPGCCNRVLGIPHSISMGYNPSLGLLEETIYVLV 348
Db      587 SRNNLVIIILGILALTFV-----TVISVP-SIDPKNVSHRVFEGATVFLLI 634
Qy      349 LDT--VGAGNGMIGFOYLSIGEL-----SLAIVIALTSGLLTALLNLKIRKA 395
Db      635 ASTFIIFAKSRPLSIITMSAVGAISVLIFFKAPADLALQFVVESTALFL-LCFYHL 693
Qy      396 PHEAKYFDDQVF 407
Db      694 PNLNRVNEKPTF 705

RESULT 12
US-09-134-001C-3105
; Sequence 3105, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
```



```
QY 254 SGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIVLGVLGLI----- 304
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 515 VDAFVPH-----ISQMHGVNPLIISIV-----IIIGLIALVNMKEVTHQ 557
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 305 -----SVGAKYLPCCNRV-----LGI 322
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 558 IIKSASITDGYRKIYREFELYSARGIRALNM--NKLNYIIMITLFIPIVAIVVGYLTVGF 615
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 323 PHSSIMGVNFSLLGLEELIYIVLVLD-----TVGAGMTGFQVLL-----SI 367
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 616 PH--VHQHLSISGFLEVLISVTLIGISLIFIRQRLTWVNLGMIGFAVTLIYFIAMKA 673
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 368 GELSLAIVALTSGLLTALLNLKIRKAPH 397
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 674 PDLALTOLVET---ITTIIFIVSFSRLPN 700
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

## RESULT 15

```
US-09-489-039A-10855
; Sequence 10855, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10855
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-10855
```

Query Match 5.2%; Score 109.5; DB 4; Length 407;

Best Local Similarity 22.2%; Pred. No. 0.0096; Matches 86; Conservative 50; Mismatches 135; Indels 117; Gaps 20;

```
QY 18 LTLFPAALILF-----YFTHYDASLEDO-----KGLVASQYV----- 50
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 18 LTLIGITITTFALGSVYTWLSLFSLSLSDKGEPIVQVAFSPGLSLGLALSSSVAKLQE 77
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 51 --GQDLTWMA--IGIGFLTSSFRHS-----WSSVAFNLFMLALGVQMAILLDGFLS 99
    ||: : : : : : : : : : : : : : : : : : : : : : : :
Db 78 RFGVKRVTVASGILLIGGFPLTA--HSSSLMMLMSAGV-LVGLADAGYLLTLNSCVK 133
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 100 QPSPGKVITLFSIWLATMSALSVLISVDVAVLCKNL-----AQLVMVVLVEVT--- 148
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 134 WPEPRKGLISAFSISGYGLSGFKPIDSHLATVGLKPTVIGATVLMVIVGATLMK 193
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 149 DLGN-----LRWVISNIFNTDYHNMNMHIYVFAAYF-----GLTVAMCLPKLPREGTE 196
    ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 194 DAPNHPRATANGVENDFTLASMRKKQYMWMLAVMFLTACMSGLYIG--VAKDIAQMV 252
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 197 DND-----QRATIPSLSAMIGALFLMFRPSVN-----SALLRSPTERK 235
    ||: : : : : : : : : : : : : : : : : : : : : : : :
Db 253 HLTVATANAAVTVISIANLGSRLVLGILSDKISRIRVITIGQVVSIVGMALLFAPL--- 309
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 236 NAVFNTRYAAVAVSVTAISGSSLAHPQ-----GKISTYGHSAVLPEGVAVDTSCHL 287
    ||: : : : : : : : : : : : : : : : : : : : : : : :
Db 310 NAL--TFEALAIACVAENFGGITTVPSLVSEPFGLNLAKNYG--VIYLGFGIGSTCG- 363
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 288 IPSPWLPVILGVLAVGLISVGAKYLPQC 315
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 364 -----SLIASLF--GGFYVTFC 378
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: March 24, 2005, 13:18:48  
Job time : 26 secs

*This Page Blank (uspro)*

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 24, 2005, 13:13:48 ; Search time 19 Seconds  
(without alignments)  
2111.705 Million cell updates/sec

Title: CAC07879

Perfect score: 2124

Sequence: 1 MSCKYPRSVRCPLCALTL.....EAKYFDQVFWKPHLAVGF 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1981	93.3	417	2	152615 gene Rhd protein -
2	1976	93.0	417	2	A46368 erythrocyte membra
3	1863	87.7	417	2	I37005 Rhesus-like protei
4	1842	86.7	417	2	I37006 Rhesus-like protei
5	1840	86.6	417	2	I37004 Rhesus-like protei
6	1833	86.3	417	2	A30405 erythrocyte membra
7	1811	85.3	417	2	I37003 Rhesus-like protei
8	1803	84.9	417	2	I37005 Rhesus-like protei
9	1509	71.0	417	2	I84434 Rhesus blood group
10	1411	66.4	354	2	S78480 Rhesus blood group
11	1294	60.9	354	2	I37053 Rhesus blood group
12	1089.5	51.3	265	2	S78479 Rhesus blood group
13	1000.5	47.1	267	2	S78478 Rhesus blood group
14	547.5	25.8	409	2	S29424 membrane glycoprot
15	412	19.4	463	2	T29442 hypotethical prote
16	361.5	17.0	457	2	T18673 hypotethical prote
17	161	7.6	44	2	PC2033 RbPI-beta polypept
18	128	6.0	475	2	T01260 probable ammonium
19	127	6.0	458	2	C82232 protom/glutamate s
20	126	5.9	421	2	B84129 ammonium transport
21	125.5	5.9	468	2	A69468 ammonium transport
22	120	5.6	537	1	F70705 hypotethical prote
23	119.5	5.6	388	2	C64722 Na+/H+-exchanging
24	119.5	5.6	394	2	AH0362 nucleoside permeas
25	119.5	5.6	424	2	B69172 cationic amino aci
26	119.5	5.6	891	2	B82495 probable MADH deny
27	119	5.6	881	2	S46633 RbPI-alpha polypep
28	118	5.6	42	2	PC2032
29	117.5	5.5	388	2	A99631 Na+/H antiporter l

30	117.5	5.5	388	2	A85482 Na+/H antiporter,
31	117.5	5.5	612	2	G64678 NADH2 dehydrogenas
32	114.5	5.4	481	2	C87435 conserved hypothec
33	114	5.4	800	2	G89831 hypotethical prote
34	113.5	5.3	333	2	E96954 Na/H antiporter (n
35	113	5.3	653	2	D82352 Iron(III) ABC tran
36	113	5.3	685	2	AC0527 ferrichrome transp
37	113	5.3	782	2	T25925 hypotethical prote
38	112.5	5.3	419	2	D64142 hypotethical prote
39	112	5.3	385	2	G82789 permease XF0589 (I
40	111.5	5.2	437	2	JC4988 high-affinity gluc
41	111.5	5.2	449	2	H69423 branched-chain ami
42	111	5.2	660	2	A64739 ferrichrome-iron t
43	110.5	5.2	438	2	AD0481 probable gluconate
44	110.5	5.2	448	2	B97907 phosphotransferase
45	110.5	5.2	612	2	E71839 NADH2 dehydrogenas

ALIGNMENTS

RESULT 1

152615 gene Rhd protein - human

C:Species: Homo sapiens (man)

C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C/Accession: 152615

R/Huang, C.H.; Reid, M.E.; Chen, Y.

A/Blood 86, 784-790, 1995

A/Title: Identification of a partial internal deletion in the RH locus causing the human

A/Reference number: 152615; MUID:95329738; PMID:7606008

A/Accession: 152615

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-417 <RBS>

A/Cross-references: UNIPROT:Q02161; GB:878509; NID:9999309; PID:AA834852.1; PID:9999310

C/Genetics:

A:Gene: Rhd

C:Superfamily: human erythrocyte membrane protein Rhd

Query Match	93.3%	Score 1981;	DB 2;	Length 417;
Best Local Similarity	95.0%;	Pred. No. 1.2e-150;		
Matches	396;	Conservative 4;	Mismatches 17;	Indels 0; Gaps 0;
QY	1	MSCKYPRSVRCPLCALTLTEAALILFPFTHYDASLEDOKGLVASYOVGODLTWMAAI	60	
DB	1	MSCKYPRSVRCPLCALTLTEAALILFPFTHYDASLEDOKGLVASYOVGODLTWMAAI	60	
QY	61	GLGFLTSSFRRHGSSVAFNLFMLALGVQWAILLDGFLSQPPSGKVITLPSIWLATMSA	120	
DB	61	GLGFLTSSFRRHGSSVAFNLFMLALGVQWAILLDGFLSQPPSGKVITLPSIWLATMSA	120	
QY	121	LSVLISVDALGVKNLAQLVVMVLVEVTDLGNRMVISNIFNTDYHNMWHIYVFAAYFG	180	
DB	121	LSVLISVDALGVKNLAQLVVMVLVEVTALGNRMVISNIFNTDYHNMWHIYVFAAYFG	180	
QY	181	LTYAWCLPKPLPGSTENDDRATIPSLAMLGALFLMFPSPVNSALLBSPTEKNAVEN	240	
DB	181	LTYAWCLPKPLPGSTENDDRATIPSLAMLGALFLMFPSPVNSALLBSPTEKNAVEN	240	
QY	241	TYAVAVSVVTALISGSSLAIPQGIKSTYGHSAVLPGGVAVDTPSCHLIPSPWLPIYVLGLV	300	
DB	241	TYAVAVSVVTALISGSSLAIPQGIKSTYGHSAVLPGGVAVDTPSCHLIPSPWLPIYVLGLV	300	
QY	301	AGLISVGAKYLPQCCNRVLGIPHSISMGYNFSLGLLEBIYIVLLVDTVGAGNGMIG	360	
DB	301	AGLISVGAKYLPQCCNRVLGIPHSISMGYNFSLGLLEBIYIVLLVDTVGAGNGMIG	360	
QY	361	FQYVLISGELSLAIVALTSGLLTALLLNKIKKAPHEACYPFDQVFWKPHLAVGF	417	
DB	361	FQYVLISGELSLAIVALTSGLLTALLLNKIKKAPHEACYPFDQVFWKPHLAVGF	417	

RESULT 2  
A46368  
erythrocyte membrane protein Rhd - human  
N/Alternate names: blood group antigen Rhd (D)  
C/Species: Homo sapiens (man)  
C/Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
A/Accession: A46368; S26564; S26561; I52581; S02085; S02087; A32509; A30216; A61174; I52  
R/Le van Kim, C.; Mourou, I.; Cherif-Zahar, B.; Raynal, V.; Cherrier, C.; Cartton, J.P.;  
Proc. Natl. Acad. Sci. U.S.A. 89, 10925-10929, 1992  
A/Title: Molecular cloning and primary structure of the human blood group Rhd polypeptid  
A/Reference number: A46368; MUID:9306356; PMID:1438298  
A/Accession: A46368  
A/Molecule type: mRNA  
A/Residues: 1-417 <LEV2>  
A/Cross-references: UNIPROT:Q02161; GB:X63097; GB:S48953; NID:936046; PIDN:CAA44811.1; F  
A/Experimental source: bone marrow, clone RhlXII  
A/Note: sequence extracted from NCBI backbone (NCIN:118725, NCBIP:118726)  
R/Le van Kim, C.; Cherif-Zahar, B.; Raynal, V.; Mourou, I.; Lopez, M.; Cartton, J.P.; Col  
Blood 80, 1074-1078, 1992  
A/Title: Multiple Rh messenger RNA isoforms are produced by alternative splicing.  
A/Reference number: S26560; MUID:92360855; PMID:1379850  
A/Accession: S26564  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-417 <LEV2>  
A/Cross-references: EMBL:X63097; GB:S48953; NID:936046; PIDN:CAA44811.1; PID:936047  
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991  
A/Accession: S26561  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-217 'M', 219-417 <LEV3>  
A/Cross-references: EMBL:X63094; NID:936027; PIDN:CAA44808.1; PID:936028  
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991  
R/Arce, M.A.; Thompson, E.S.; Wagner, S.; Coyne, K.E.; Ferdman, B.A.; Lublin, D.M.  
Blood 82, 651-655, 1993  
A/Title: Molecular cloning of Rhd cDNA derived from a gene present in Rhd-positive, but  
A/Reference number: I52581; MUID:93320449; PMID:8329718  
A/Accession: I52581  
A/Status: preliminary; translated from GB/EMBL/DBD  
A/Molecule type: protein  
A/Residues: 1-217 'M', 219-417 <RES>  
A/Cross-references: GB:I08429; NID:9337390; PIDN:AAA02679.1; PID:9337391  
R/Avent, N.D.; Ridgwell, K.; Mabry, W.J.A.; Ametee, D.J.; Kumpel, B.  
Biochem. J. 256, 1043-1046, 1988  
A/Title: Protein-sequence studies on Rh-related polypeptides suggest the presence of at  
A/Reference number: S02085; MUID:89134163; PMID:3146980  
A/Accession: S02085  
A/Molecule type: protein  
A/Residues: 2-11 'X', 13-33 <AVE1>  
A/Note: this peptide was designated blood group Rh-related protein D30  
A/Accession: S02087  
A/Molecule type: protein  
A/Residues: 2-11 'X', 13-14 <AVE2>  
A/Note: this peptide was designated blood group Rh-related protein R6A32  
R/Bloy, C.; Blanchard, D.; Dahr, W.; Beyreuther, K.; Salmon, C.; Cartton, J.P.  
Blood 72, 661-666, 1988  
A/Title: Determination of the N-terminal sequence of human red cell Rh(D) polypeptide an  
A/Reference number: A32509; MUID:88294325; PMID:3135863  
A/Accession: A32509  
A/Molecule type: protein  
A/Residues: 2-11 'L', 13-15 'X', 17 <BLO>  
R/Saboort, A.M.; Smith, B.L.; Agre, P.  
Proc. Natl. Acad. Sci. U.S.A. 85, 4042-4045, 1988  
A/Title: Polymorphism in the M-r 32,000 Rh protein purified from Rh(D)-positive and -neg  
A/Reference number: A30216; MUID:88234555; PMID:3131772  
A/Accession: A30216  
A/Molecule type: protein  
A/Residues: 2-11 'X', 13-21 <SAB>  
R/Suyama, K.; Goldstein, J.; Abersold, R.; Kent, S.  
Blood 77, 411, 1991  
A/Title: Regarding the size of Rh proteins.  
A/Reference number: A61174; MUID:91091537; PMID:1898705  
A/Accession: A61174

A/Molecule type: protein  
A/Residues: 401-407 'DI' <SU7>  
R/Westhoff, C.M.; Wylie, D.E.  
Blood 83, 3098-3100, 1994  
A/Title: Identification of a new Rhd-specific mRNA from K562 cells.  
A/Reference number: I52589; MUID:94235883; PMID:8180407  
A/Accession: I52589  
A/Status: preliminary; translated from GB/EMBL/DBD  
A/Molecule type: mRNA  
A/Residues: 1-217 'M', 219-313, 410-417 <RE2>  
A/Cross-references: GB:S70174; NID:9546725; PIDN:AAB30756.1; PID:9546726  
R/Suyama, K.; Lunn, R.; Haller, S.; Goldstein, J.  
Blood 84, 1975-1981, 1994  
A/Title: Rh(D) antigen expression and isolation of a new Rh(D) cDNA isoform in human ery  
A/Reference number: I52596; MUID:94362249; PMID:8080999  
A/Accession: I52596  
A/Status: preliminary; translated from GB/EMBL/DBD  
A/Molecule type: mRNA  
A/Residues: 1-217 'M', 219-313, 'V', 315 'S' <RE3>  
A/Cross-references: GB:S73913; NID:9693866; PIDN:AAB31911.1; PID:9693867  
C/Genetics:  
A/Gene: GDB:RHD; RH; RHD  
A/Cross-references: GDB:119551; OMIM:111680  
A/Map position: 1p36.2-1p34  
C/Superfamily: human erythrocyte membrane protein Rhd  
C/Keywords: erythrocyte; surface antigen; transmembrane protein  
  
Query Match 93.0%; Score 1976; DB 2; Length 417;  
Best Local Similarity 95.0%; Pred. No. 36-150;  
Matches 396; Conservative 4; Mismatches 17; Indels 0; Gaps 0;  
  
QY 1 MSCKYRSVORCLP/CATLREAAALLLPFFPHYDASLEDOGLVASTVQVQGLTWMAI 60  
DB 1 MSCKYRSVORCLP/MALTLREALLLPFFPHYDASLEDOGLVASTVQVQGLTWMAI 60  
QY 61 GLGFLTSPFRHSWSVAFNLFMLALGVQWAILLDGFLSOPFSKGVITLPSIWLATMSA 120  
DB 61 GLGFLTSPFRHSWSVAFNLFMLALGVQWAILLDGFLSOPFSKGVITLPSIWLATMSA 120  
QY 121 LSVLISVDVAVLGNLAQIVWVWVLEVDLGNLRVNSINFTVDYHMMMHIIYPAAYFG 180  
DB 121 LSVLISVDVAVLGNLAQIVWVWVLEVDLGNLRVNSINFTVDYHMMMHIIYPAAYFG 180  
QY 181 LTVNACLPEKPEGEENDORATIPSLSAMGALFIWMFRSVNSALLRSIERKNVFN 240  
DB 181 LTVNACLPEKPEGEENDORATIPSLSAMGALFIWMFRSVNSALLRSIERKNVFN 240  
QY 241 TYAAVAVSVTAISGSSIAHPQGIKSTYGHSAVLPBGAVDTSCHLIPSPWLPVGLV 300  
DB 241 TYAAVAVSVTAISGSSIAHPQGIKSTYGHSAVLPBGAVDTSCHLIPSPWLPVGLV 300  
QY 301 AGLISVRGAKYLPGCCNNVLDGIPHSISGYNFSLILGIELIIVLVLDVVGAGNMIG 360  
DB 301 AGLISVRGAKYLPGCCNNVLDGIPHSISGYNFSLILGIELIIVLVLDVVGAGNMIG 360  
QY 361 FOVLISIGELSLAIVALTSGLTALLNLTKIRKAPHEAKYFDQVWPKPFLAVGF 417  
DB 361 FOVLISIGELSLAIVALTSGLTALLNLTKIRKAPHEAKYFDQVWPKPFLAVGF 417  
  
RESULT 3  
137005  
Rhesus-like protein - chimpanzee  
C/Species: Pan troglodytes (chimpanzee)  
C/Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 09-Jul-2004  
R/Salvignol, I.; Blancher, A.; Calvas, P.; Clayton, J.; Socha, W.W.; Colin, Y.; Ruffie, C.  
Biochem. Genet. 32, 201-221, 1994  
A/Title: Molecular genetics of chimpanzee Rh-related genes: their relationship with the f  
A/Reference number: I37003; MUID:95085595; PMID:7993735  
A/Accession: I37005  
A/Status: preliminary; translated from GB/EMBL/DBD  
A/Molecule type: mRNA

A:Residues: 1-417 <RES>  
 A:Cross-references: UNIPROT:Q28814; GB:L37050; NID:g606991; PID:AAA65624.1; PID:g606992  
 C:Superfamily: human erythrocyte membrane protein Rhd

Query Match 87.7%; Score 1863; DB 2; Length 417;  
 Best Local Similarity 89.2%; Pred. No. 3.2e-141;  
 Matches 372; Conservative 12; Mismatches 33; Indels 0; Gaps 0;

QY 1 MSCKYPRSVQRCLPLCALTEEAAILLFYFPTHYDASLEDDKGLVASVYQGDLTWAAI 60  
 DB 1 MSCKYPRSVQRCLPLCALTEEAAILLFYFPTHYDASLEDDKGLVASVYQGDLTWAAI 60  
 QY 61 GLGFLTSSFRHSHSSVAFLFMLALGVQMAILLDGLSOPPGSKVITLFSIRLATMSA 120  
 DB 61 GLGFLTSSFRHSHSSVAFLFMLALGVQMAILLDGLSOPPGSKVITLFSIRLATMSA 120  
 QY 121 LSVLISVDALVAGKVNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNMHIYVFAAYFG 180  
 DB 121 LSVLISVDALVAGKVNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNMHIYVFAAYFG 180  
 QY 181 LTVAMCLPKPLPEGTEDNDQRAITPSLSAMLGALFLMFRPSVNSALLRSPIERKNAVF 240  
 DB 181 LTVAMCLPKPLPKETEDKQDIAITPSLSAMLGALFLMFRPSVNSALLRSPIERKNAVF 240  
 QY 241 TYVAVASVVTATISGSSLAHPQGIKSTYGHSAVLPGVAADTSGHLIPSPWLPYVLGLV 300  
 DB 241 TYVAVASVVTATISGSSLAHPQGIKSTYGHSAVLPGVAADTSGHLIPSPWLPYVLGLV 300  
 QY 301 AGLISVGAKYLPCCNCRVLGIPHSSIMGVNFSLLGLLEIYIVLLVLDTVGAGNMIG 360  
 DB 301 AGLISVGAKYLPCCNCRVLGIPHSSIMGVNFSLLGLLEIYIVLLVLDTVGAGNMIG 360  
 QY 361 FOVLISIGELSLAIVIALTSGLLTALLNLKIRKAPHEAKYFPDQVFWKPHLAVGF 417  
 DB 361 FOVLIRIGESLATTIALTSGLLTALLNLKIRKAPHEAKYFPDQVFWKPHLAVGF 417

## RESULT 4

137076  
 Rhesus-like protein - gorilla  
 C:Species: Gorilla gorilla (gorilla)  
 C>Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 09-Jul-2004  
 C:Accession: I37076  
 R:Salvignol, I.; Blancher, A.; Calvas, P.; Clayton, J.; Socha, W.W.; Colin, Y.; Ruffie, Biochem. Genet. 32, 201-221, 1994  
 A:Title: Molecular genetics of chimpanzee Rh-related genes: their relationship with the A:Reference number: I37003; MUID:95085595; PMID:7993375  
 A:Accession: I37076  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-417 <RES>  
 A:Cross-references: UNIPROT:Q28427; GB:L37053; NID:g607011; PID:AAA65627.1; PID:g607012  
 C:Superfamily: human erythrocyte membrane protein Rhd

Query Match 86.7%; Score 1842; DB 2; Length 417;  
 Best Local Similarity 89.0%; Pred. No. 1.5e-139;  
 Matches 371; Conservative 11; Mismatches 35; Indels 0; Gaps 0;

QY 1 MSCKYPRSVQRCLPLCALTEEAAILLFYFPTHYDASLEDDKGLVASVYQGDLTWAAI 60  
 DB 1 MSCKYPRSVQRCLPLCALTEEAAILLFYFPTHYDASLEDDKGLVASVYQGDLTWAAI 60  
 QY 61 GLGFLTSSFRHSHSSVAFLFMLALGVQMAILLDGLSOPPGSKVITLFSIRLATMSA 120  
 DB 61 GLGFLTSSFRHSHSSVAFLFMLALGVQMAILLDGLSOPPGSKVITLFSIRLATMSA 120  
 QY 121 LSVLISVDALVAGKVNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNMHIYVFAAYFG 180  
 DB 121 LSVLISVDALVAGKVNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNMHIYVFAAYFG 180  
 QY 181 LTVAMCLPKPLPEGTEDNDQRAITPSLSAMLGALFLMFRPSVNSALLRSPIERKNAVF 240  
 DB 181 LTVAMCLPKPLPKETEDKQDIAITPSLSAMLGALFLMFRPSVNSALLRSPIERKNAVF 240

QY 241 TYVAVASVVTATISGSSLAHPQGIKSTYGHSAVLPGVAADTSGHLIPSPWLPYVLGLV 300  
 DB 241 TYVAVASVVTATISGSSLAHPQGIKSTYGHSAVLPGVAADTSGHLIPSPWLPYVLGLV 300  
 QY 301 AGLISVGAKYLPCCNCRVLGIPHSSIMGVNFSLLGLLEIYIVLLVLDTVGAGNMIG 360  
 DB 301 AGLISVGAKYLPCCNCRVLGIPHSSIMGVNFSLLGLLEIYIVLLVLDTVGAGNMIG 360  
 QY 361 FOVLISIGELSLAIVIALTSGLLTALLNLKIRKAPHEAKYFPDQVFWKPHLAVGF 417  
 DB 361 FOVLIRIGESLATTIALTSGLLTALLNLKIRKAPHEAKYFPDQVFWKPHLAVGF 417

## RESULT 5

137004  
 Rhesus-like protein - chimpanzee  
 C:Species: Pan troglodytes (chimpanzee)  
 C>Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 09-Jul-2004  
 C:Accession: I37004  
 R:Salvignol, I.; Blancher, A.; Calvas, P.; Clayton, J.; Socha, W.W.; Colin, Y.; Ruffie, Biochem. Genet. 32, 201-221, 1994  
 A:Title: Molecular genetics of chimpanzee Rh-related genes: their relationship with the A:Reference number: I37003; MUID:95085595; PMID:7993375  
 A:Accession: I37004  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-417 <RES>  
 A:Cross-references: UNIPROT:Q28813; GB:L37049; NID:g606989; PID:AAA65623.1; PID:g606990  
 C:Superfamily: human erythrocyte membrane protein Rhd

Query Match 86.6%; Score 1840; DB 2; Length 417;  
 Best Local Similarity 88.7%; Pred. No. 2.2e-139;  
 Matches 370; Conservative 11; Mismatches 36; Indels 0; Gaps 0;

QY 1 MSCKYPRSVQRCLPLCALTEEAAILLFYFPTHYDASLEDDKGLVASVYQGDLTWAAI 60  
 DB 1 MSCKYPRSVQRCLPLCALTEEAAILLFYFPTHYDASLEDDKGLVASVYQGDLTWAAI 60  
 QY 61 GLGFLTSSFRHSHSSVAFLFMLALGVQMAILLDGLSOPPGSKVITLFSIRLATMSA 120  
 DB 61 GLGFLTSSFRHSHSSVAFLFMLALGVQMAILLDGLSOPPGSKVITLFSIRLATMSA 120  
 QY 121 LSVLISVDALVAGKVNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNMHIYVFAAYFG 180  
 DB 121 LSVLISVDALVAGKVNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNMHIYVFAAYFG 180  
 QY 181 LTVAMCLPKPLPEGTEDNDQRAITPSLSAMLGALFLMFRPSVNSALLRSPIERKNAVF 240  
 DB 181 LTVAMCLPKPLPKETEDKQDIAITPSLSAMLGALFLMFRPSVNSALLRSPIERKNAVF 240  
 QY 241 TYVAVASVVTATISGSSLAHPQGIKSTYGHSAVLPGVAADTSGHLIPSPWLPYVLGLV 300  
 DB 241 TYVAVASVVTATISGSSLAHPQGIKSTYGHSAVLPGVAADTSGHLIPSPWLPYVLGLV 300  
 QY 301 AGLISVGAKYLPCCNCRVLGIPHSSIMGVNFSLLGLLEIYIVLLVLDTVGAGNMIG 360  
 DB 301 AGLISVGAKYLPCCNCRVLGIPHSSIMGVNFSLLGLLEIYIVLLVLDTVGAGNMIG 360  
 QY 361 FOVLISIGELSLAIVIALTSGLLTALLNLKIRKAPHEAKYFPDQVFWKPHLAVGF 417  
 DB 361 FOVLIRIGESLATTIALTSGLLTALLNLKIRKAPHEAKYFPDQVFWKPHLAVGF 417

## RESULT 6

A30405  
 erythrocyte membrane protein Rh (unknown specificity) - human  
 N:Alternate names: blood group Rh antigen  
 C:Species: Homo sapiens (man)  
 C>Date: 05-Oct-1990 #sequence\_revision 05-Oct-1990 #text\_change 09-Jul-2004  
 C:Accession: A30405; S13060; I54273; S40515; S40517; S02085; S02087; A32509; A307; R:Cherif-Zahar, B.; Bloy, C.; Le Van Kim, C.; Blanchard, D.; Bailly, P.; Hermand, P.; Sai Proc. Natl. Acad. Sci. U.S.A. 87, 6243-6247, 1990

A>Title: Molecular cloning and protein structure of a human blood group Rh polypeptide.  
 A/Reference number: A30405; MUID:90349591; PMID:1696722  
 A/Accession: A30405  
 A/Molecule type: mRNA  
 A/Residues: 1-417 <CHR>  
 A/Cross-references: UNIPROT:P18577; GB:M34015; NID:G337398; PIDN:AAA36567.1; PID:G337398  
 R/Avent, N.D.; Ridgwell, K.; Tanner, M.J.A.; Anstee, D.J.  
 Biochem. J. 271, 821-825, 1990  
 A/Title: cDNA cloning of a 30 kDa erythrocyte membrane protein associated with Rh (Rhesu  
 A/Reference number: S13060; MUID:91058522; PMID:2123099  
 A/Accession: S13060  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-417 <AVE1>  
 A/Cross-references: EMBL:X54534; NID:G36017; PIDN:CAA38401.1; PID:G36018  
 R/Kajli, E.; Umenishi, F.; Iwamoto, S.; Ikemoto, S.  
 Hum. Genet. 91, 157-162, 1993  
 A/Title: Isolation of a new cDNA clone encoding an Rh polypeptide associated with the Rh  
 A/Reference number: I54273; MUID:93216282; PMID:7916743  
 A/Accession: I54273  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-417 <RES>  
 A/Cross-references: GB:S57967; NID:G299049; PIDN:AAE26080.1; PID:G299050  
 R/Mouro, I.; Collin, Y.; Cherif-Zahar, B.; Cartrom, J.P.; Le van Kim, C.  
 Nature Genet. 5, 62-65, 1993  
 A/Title: Molecular genetic basis of the human Rhesus blood group system.  
 A/Reference number: S40515; MUID:94035121; PMID:8220426  
 A/Accession: S40515  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-301, 'F', 303-417 <MOU1>  
 A/Accession: S40516  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-225, 'A', 227-301, 'F', 303-417 <MOU2>  
 A/Accession: S40517  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-15, 'C', 17-59, 'I', 61-67, 'S', 69-102, 'S', 104-225, 'A', 227-301, 'F', 303-417 <MO3  
 R/Avent, N.D.; Ridgwell, K.; Mabdy, W.J.; Tanner, M.J.A.; Anstee, D.J.; Kumpel, B.  
 Biochem. J. 256, 1043-1046, 1988  
 A/Title: Protein-sequence studies on Rh-related polypeptides suggest the presence of at  
 A/Reference number: S02085; MUID:89134163; PMID:3146980  
 A/Accession: S02085  
 A/Molecule type: protein  
 A/Residues: 2-11, 'X', 13-33 <AVE2>  
 A/Note: this peptide was designated blood group Rh-related protein D30  
 A/Accession: S02087  
 A/Molecule type: protein  
 A/Residues: 2-11, 'X', 13-14 <AVE3>  
 R/Bloy, C.; Blanchard, D.; Dahr, W.; Beyreuther, K.; Salmon, C.; Cartrom, J.P.  
 Blood 72, 661-666, 1988  
 A/Title: Determination of the N-terminal sequence of human red cell Rh(D) polypeptide an  
 A/Reference number: A32509; MUID:88294325; PMID:3135863  
 A/Accession: A32509  
 A/Molecule type: protein  
 A/Residues: 2-11, 'L', 13-15, 'X', 17 <BLO>  
 R/Saboori, A.M.; Smith, B.L.; Agre, P.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 4042-4045, 1988  
 A/Title: Polymorphism in the M-r 32,000 Rh protein purified from Rh(D)-positive and -neg  
 A/Reference number: A30216; MUID:88234555; PMID:3131772  
 A/Accession: A30216  
 A/Molecule type: protein  
 A/Residues: 2-11, 'X', 13-21 <SAB>  
 R/Suyama, K.; Goldstein, J.; Aebersold, R.; Kent, S.  
 Blood 77, 411, 1991  
 A/Title: Regarding the size of Rh proteins.  
 A/Reference number: A61174; MUID:91091537; PMID:1698705  
 A/Accession: A61174  
 A/Molecule type: protein  
 A/Residues: 401-407, 'DI' <SUY>

C/Superfamily: human erythrocyte membrane protein Rhd  
 C/Keywords: alternative splicing; erythrocyte; surface antigen; transmembrane protein

Query Match 86.3%; Score 1833; DB 2; Length 417;

Best Local Similarity 88.7%; Pred. No. 7.9e-139;

Matches 370; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

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Db      1 MSCKYPSVORCLPLCALTLLEAALLLFFPETHYDASLEDOKGLVASVYQGDLTWMAI 60
QY      61 GLGFLTSSFRRHSSVAFFLFWALGVQWAILLDGFLSQFPFGKVITLFSIRLATMSA 120
      61 GLGFLTSSFRRHSSVAFFLFWALGVQWAILLDGFLSQFPFGKVITLFSIRLATMSA 120
Db      61 GLGFLTSSFRRHSSVAFFLFWALGVQWAILLDGFLSQFPFGKVITLFSIRLATMSA 120
QY      121 LSVLISYDAVLGKVNLAQLVWVLVEVTDGLNRMVINSINFTDYMNMNHIVFAAYFG 180
      121 LSVLISYDAVLGKVNLAQLVWVLVEVTDGLNRMVINSINFTDYMNMNHIVFAAYFG 180
Db      121 MSVLISAGAVLGKVNLAQLVWVLVEVTDGLNRMVINSINFTDYMNMNHIVFAAYFG 180
QY      181 LTVAMCLPKPLPEGTEDNDORATIPSLSMGLALFLMFRPSVNSALLRSPIERKNAVEN 240
      181 LTVAMCLPKPLPEGTEDNDORATIPSLSMGLALFLMFRPSVNSALLRSPIERKNAVEN 240
Db      181 LTVAMCLPKPLPEGTEDNDORATIPSLSMGLALFLMFRPSVNSALLRSPIERKNAVEN 240
QY      241 TYAAVAVSVYTTAISGSLAHPOGKISKTYGSHAVLPEGVAVDTSCHLTSPFWLPTVLGLV 300
      241 TYAAVAVSVYTTAISGSLAHPOGKISKTYGSHAVLPEGVAVDTSCHLTSPFWLPTVLGLV 300
Db      241 TYAAVAVSVYTTAISGSLAHPOGKISKTYGSHAVLPEGVAVDTSCHLTSPFWLPTVLGLV 300
QY      301 AGLISVGAKEYLPGCCNRYLGIPIHSGIMGNFSLGLEELIYIVLVLDVTGANGMIG 360
      301 AGLISVGAKEYLPGCCNRYLGIPIHSGIMGNFSLGLEELIYIVLVLDVTGANGMIG 360
Db      301 AGLISVGAKEYLPGCCNRYLGIPIHSGIMGNFSLGLEELIYIVLVLDVTGANGMIG 360
QY      361 FOVLISIGLSLAIYALVLTSLGLTLNLTKRKAPHEAKYRDDDOYFWKFEHLAVGF 417
      361 FOVLISIGLSLAIYALVLTSLGLTLNLTKRKAPHEAKYRDDDOYFWKFEHLAVGF 417
Db      361 FOVLISIGLSLAIYALVLTSLGLTLNLTKRKAPHEAKYRDDDOYFWKFEHLAVGF 417

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#### RESULT 7

137003 Rhesus-like protein - chimpanzee

C/Species: Pan troglodytes (chimpanzee)

C/Date: 04-Oct-1996 #sequence revision 04-Oct-1996 #text\_change 09-Jul-2004

C/Accession: I37003

R/salvignol, I.; Blancher, A.; Calvas, P.; Clayton, J.; Socha, W.W.; Collin, Y.; Ruffie, C.

Biochem. Genet. 32, 201-221, 1994

A/Title: Molecular genetics of chimpanzee Rh-related genes: their relationship with the f

A/Reference number: I37003; MUID:95085595; PMID:7993375

A/Accession: I37003

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-417 <RES>

A/Cross-references: UNIPROT:Q28812; GB:I37048; NID:G606987; PIDN:AAA65622.1; PID:G606988

C/superfamily: human erythrocyte membrane protein RHD

Query Match 85.3%; Score 1811; DB 2; Length 417;

Best Local Similarity 87.5%; Pred. No. 4.5e-137;

Matches 365; Conservative 11; Mismatches 41; Indels 0; Gaps 0;

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      1 MSCKYPSVORCLPLCALTLLEAALLLFFPETHYDASLEDOKGLVASVYQGDLTWMAI 60
Db      1 MSCKYPSVORCLPLCALTLLEAALLLFFPETHYDASLEDOKGLVASVYQGDLTWMAI 60
QY      61 GLGFLTSSFRRHSSVAFFLFWALGVQWAILLDGFLSQFPFGKVITLFSIRLATMSA 120
      61 GLGFLTSSFRRHSSVAFFLFWALGVQWAILLDGFLSQFPFGKVITLFSIRLATMSA 120
Db      61 GLGFLTSSFRRHSSVAFFLFWALGVQWAILLDGFLSQFPFGKVITLFSIRLATMSA 120
QY      121 LSVLISYDAVLGKVNLAQLVWVLVEVTDGLNRMVINSINFTDYMNMNHIVFAAYFG 180
      121 LSVLISYDAVLGKVNLAQLVWVLVEVTDGLNRMVINSINFTDYMNMNHIVFAAYFG 180
Db      121 LSVLISYDAVLGKVNLAQLVWVLVEVTDGLNRMVINSINFTDYMNMNHIVFAAYFG 180
QY      181 LTVAMCLPKPLPEGTEDNDORATIPSLSMGLALFLMFRPSVNSALLRSPIERKNAVEN 240
      181 LTVAMCLPKPLPEGTEDNDORATIPSLSMGLALFLMFRPSVNSALLRSPIERKNAVEN 240
Db      181 LTVAMCLPKPLPEGTEDNDORATIPSLSMGLALFLMFRPSVNSALLRSPIERKNAVEN 240

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```

Qy      241  TTYVAASVWTAIASSSLAHPOGKISKYGGSAVLPEVAADTCHLIPSPWMLPIYGLV 300
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241  TTYTAAASVWTAIASSSLAHPOGKISMTYVASVAVLGAAGVGTCHLIPSPMLAMVGLV 300
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      301  AGLISVRGAKTLPGCCNPNVLGIPIHSSINGVNFSLIGLEETIYVLVLDTVNGAGNMIG 360
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      301  AGLISIGGAKGPGCCNPNVLGIPISSVNHYNFSLIGLEETIYVLVVRHVTWNGNMIG 360
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      361  FOVLSTIGELSLATYIATLTSGLTTLTLNLTIKRAPHEAKYFDQVFWKPFHLAVGF 417
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      361  FOVLSTIGELSLATIAITLTSGLTGLTLNLTKRPAHVAKYSDQVFWKPFHLAVGF 417
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
I37075
Rheus-11ke protein - gorilla
C:Species: Gorilla gorilla (Gorilla)
C:Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004
C:Accession: I37075
R:Salvignol, I.; Blancher, A.; Calvas, P.; Clayton, J.; Socha, W.W.; Colin, Y.; Ruffie,
Biochem. Genet. 32, 201-221, 1994
A:Title: Molecular genetics of chimpanzee Rh-related genes: their relationship with the
A:Reference number: I37003; MUID:95085595; PMID:7993375
A:Accession: I37075
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-417 <RES>
C:Superfamily: human erythrocyte membrane protein RND
C:Superfamily: human erythrocyte membrane protein RND

```

```

Query Match 361; Score 1803; DB 2; Length 417;
Best Local Similarity 86.6%; Pred. No. 26-136;
Matched 361; Conservative 15; Mismatches 41; Indels 0; Gaps 0;

QY 1 MSCKYPRSVORCLPLCALTLLENALITLFFFTTHDASLEDDKGLVASVYQGDITVMAAI 60
DB 1 MSSKYPRSVORCLPLCALTLLENALITLFFFTTHDASLEDDKGLVASVYQGDITVMAAI 60
QY 61 GLGLPITSPFRHRSWSVAFNLFMLALGVQMAILLDGLFSOPPSGQVITLPSILATMSA 120
DB 61 GFGFLTSSFRHRSWSVAFNLFMLALGVQMAILLDGLFSOPPSGQVITLPSILATMSA 120
QY 121 LSVLISVAVLGGKVAQLQVNVVLVEVTDLNLKRVISINFTDYMNMMAIYYFAAFVG 180
DB 121 LSVLISAVAVLGGYVNLVDLVNVVLVEVYALGTMKRVININFTDYMNMHTFYFAAFVG 180
QY 181 LTVAMCKLPRLPEGTEDNDQRATIPSLISAMLGALFLMFRPSVNSALLRSPIERKNAVN 240
DB 181 VTVAMCKLPKPLDIKEDKQIATIPSLISAMGLFLMFWPSPNSALLRSPIERKNAVFN 240
QY 241 TYVAAVSVVTVRAISSSLAHPOGKISKTYGSAVLPEVAADTSGHLIPSWMLPIYGLV 300
DB 241 TYVAALVSVTVRAISSSLAHPOGKINMTYMNNAVLAVGVAAGTSGHLLTSPWMLMVLGLV 300
QY 301 AGLISVRGAKYLPGCCNRRVLGIPIHSSIMGYNFSLGLLEEIIYIVLLVLDVPGAGNGMG 360
DB 301 AGLISIGAKKCLPGCCNNRVLGIHDSVWHYNFSLGLGELTIYIVLWHLTVGAGNGMGV 360
QY 361 FOVLSTIELSLAIVIALTSGLLTALLNLKRAKPEAKYPPDDQVFWKPFHLAVGF 417
DB 361 FOVLSTGELSLAIALAVTSGLLTGLLNLKIMKAPHAAKYPPDDQVFWKPFHLAVGF 417

RESULT 9
184434
Rhesus-like protein - crab-eating macaque
CISpecies: Macaca fascicularis (crab-eating macaque)
CDate: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
CAccession: I84434
R:SaliVigMOL, I.; Blancher, A.; Calyas, P.; Clayton, J.; Socha, W.W.; Colin, Y.; Ruffie,
Biochem. Genet. 32, 201-221, 1994
Article: Molecular genetics of chimpanzee Rh-related genes: their relationship with the
A:Reference number:137003; WUID:95085595; PMID:7993375

```

A1:Accession: I84434  
A1:Status: preliminary; translated from GB/EMBL/DBJ  
A1:Molecule type: mRNA  
A1:Residues: 1-417 <RES>  
A1:Cross-references: UNIPROT:Q28481; GB:L37054; NID:g609515; PIDN:AAA65628.1; PID:g609516  
C1:Superfamily: human erythrocyte membrane protein RhD

```

Query Match 71.0%; Score 1509; DB 2; Length 417,
Best Local Similarity 74.3%; Pred. No. 6e-113;
Matches 310; Conservative 31; Mismatches 76; Indels 0; Gaps 0;

QY 1 MSCKRPSVORCLPCLALTLLEAALLLFFEFTHYDASLEDOQLVASVYOGDLYTMAAI 60
DB 1 MSKXPRSVRCCLPEMLATLEAALLLFFEFTHYDASLEDOQGLVASVYOCODLTMAVL 60
QY 61 GLGLTLSSPFRHSMSSVAENLFLMALGVOMAILLDGLSGFPSPGKVVITLFSTLWTMSA 120
DB 61 GLGFETSNLRNRSWSSVAENLFLTALGVOMAILLDGLSGFSPGKVVIKLFSRLRLRST 120
QY 121 LSTVLSYDAVLGKKNLALQLVVNLVEVTDGNTLRMVISINFTPDYHNMNMHIYFAAYFG 180
DB 121 TSMLSINMNAVLGKKNLALQLVVNLVEVLTGTGTRIVYINFKLDYGNMNMHIHFAAYFG 180
QY 181 LTVAMCLPKPLPBGTEEDNDQRAITPSLSAMLGALFLMFRPSVNSALLRSPIERKAAVEN 240
DB 181 LTVAMCLPKPLPKTEBERKYOTTSPSLPAMLGTLFLMFMPTFNSALLNPIERKAAVFS 240
QY 241 TYVVAIVASVYATISGSSLAHPQGLISKTYGHSANLPEGVAVVDNSCHLIPSPMLPIYGLV 300
DB 241 TYVVAIVASVYATISVSSLAHPQRKINMTYPMNGLAGVAVVGSCHVHSBPMIAVNLGLV 300
QY 301 AGLISVGAKEYPGCCNRVLGIPIHSSIMGVNFSLGLLBEIYIVLVLDPTVGANGMIG 360
DB 301 AGLISFGAKCLPYCCFNRVLGIHSHSHMHTFGPLALLGEITYIVLMALAVFAMSSNMIG 360
QY 361 FOVLISIGELSLAIVLITSGLTALLLNKIRAAPIEAKYPPDDQVWKKRPHLAVGF 417
DB 361 FOVLISIGTSLAIAAMSITGGLTLGLLNKIKWGGPVAVYFPDQAAWBEPPHLAVGF 417

```

RESULT 10  
 S78480  
 Rhesus blood group antigen-like protein isoform 4 - human  
 C|Species: Homo sapiens (man)  
 C|Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 15-Jun-2001  
 C|Accession: S78480; S26560  
 R|Colln. Y.  
 submitted to the EMBL Data Library, November 1991  
 A|Reference number: S78478  
 A|Accession: S78480  
 A|Molecule type: mRNA  
 A|Residues: 1-354 <CDL>  
 A|Cross-references: EMBL:X63098; NID:G36019; PIDN:CAA44812.1; PID:G36020  
 R|Le Van Kim, C.; Cherif-Zahar, B.; Raynal, V.; Mouru, I.; Lopez, M.; Cartron, J.P.; Col  
 Blood 80, 1074-1078, 1992  
 A|Title: Multiple Rh messenger RNA isoforms are produced by alternative splicing.  
 A|Reference number: S26560; MUID:92360855; PMID:1379850  
 A|Accession: S26560  
 A|Molecule type: mRNA  
 A|Residues: 160-354 <LEV>  
 A|Cross-references: EMBL:X63098  
 A|Experimental source: tissue-type bone marrow  
 C|Superfamily: human erythrocyte membrane protein RhD  
 C|Keywords: alternative splicing; erythrocyte; surfact antigen; transmembrane protein

Query Match	Similarity	Score 1411	DB 2	Length 354
Best Local	Similarity 90.18	Pred. No. 3.3e-105		
Matches 282	Conservative 10	Mismatches 21	Indels 0	Gaps 0

Qy	1	MSCKYPSVQCFPLCATTEAAILLPFFPHYDASLEDDQGLVASVYQGGDTITVAAT	60
Db	1	MSKYYPSVSRCTPLCATTEAAILLPFFPHYDASLEDDQGLVASVYQGGDTITVAAL	60

```

QY 61 GIGFLTSPRRHSSWSVAENLFMLALGVOMAILLDGFLSQPPSGKVITLPSIMLATMSA 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 CIGFLTSPRRHSSWSVAENLFMLALGVOMAILLDGFLSQPPSGKVITLPSIRLATMSA 120
QY 121 LSVLISVDVAVLGKVNLAQLVWVVLVEVTDLGNIIRWVINSIFNTDYHMMNMHIYVFAAYFG 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 MSVLISAGAVLGKVNLAQLVWVVLVEVTDLGTLRWVINSIFNTDYHMMNRHYVFAAYFG 180
QY 181 LTVAMCLPKPLPEGTEDNDORATIPSLSAMLGALFLMFRPSVNSALIRSPIERKNAVEN 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LTVAMCLPKPLPEGTEDNDORATIPSLSAMLGALFLMFRPSVNSALIRSPIORKNAMEN 240
QY 241 TYVAVAVSVTVAISGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIVLGLV 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 TYVAVAVSVTVAISGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIVLGLV 300
QY 301 AGLISVRGAKYLP 313
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 AGLISIGAKCLP 313
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 11  
137053  
Rhesus-like protein - piliated gibbon  
C/Species: Hylobates pileatus (piliated gibbon)  
C/Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 09-Jul-2004  
C/Accession: 137053  
R/Salvignol, I.; Blancher, A.; Calvas, P.; Clayton, J.; Socha, W.W.; Collin, Y.; Ruffie, Biochem. Genet. 32, 201-221, 1994  
A/Title: Molecular genetics of chimpanzee Rh-related genes: their relationship with the A/Reference number: 137003; MUID:9508595; PMID:7993375  
A/Accession: 137053  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-354 <RES>  
A/Cross-references: UNIPROT:Q28446; GB:137051; NID:9607007; PIDN:AAA65625.1; PID:9607008  
C/Superfamily: human erythrocyte membrane protein Rhd

```

Query Match 60.9%; Score 1294; DB 2; Length 354;
Best Local Similarity 82.7%; Pred. No. 7,4e-96;
Matches 259; Conservative 20; Mismatches 34; Indels 0; Gaps 0;

QY 1 MSCKPSRYORCLPICALTLTEAALILFFFTTHDASLEDQGLVASVYOGDITVMAAI 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MSSKTPSVRCCLPLMALTEAALILFFFTTHDASLEDQGLVATYQVGDITVMAAL 60
QY 61 GIGFLTSPRRHSSWSVAENLFMLALGVOMAILLDGFLSQPPSGKVITLPSIMLATMSA 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GIGFLTSPRRHSSWSVAENLFMLALGVOMAILLDGFLSQPPSGKVITLPSIRLATMSA 120
QY 121 LSVLISVDVAVLGKVNLAQLVWVVLVEVTDLGNIIRWVINSIFNTDYHMMNMHIYVFAAYFG 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 MSVLISAGAVLGKVNLAQLVWVVLVEVTDLGTLRWVINSIFNTDYHMMNRHYVFAAYFG 180
QY 181 LTVAMCLPKPLPEGTEDNDORATIPSLSAMLGALFLMFRPSVNSALIRSPIERKNAVEN 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LTVAMCLPKPLPEGTEDNDORATIPSLSAMLGALFLMFRPSVNSALIRSPIERKNAVEN 240
QY 241 TYVAVAVSVTVAISGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIVLGLV 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 TYVAVAVSVTVAISGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIVLGLV 300
QY 301 AGLISVRGAKYLP 313
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 AGLISIGAKCLP 313
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 12  
S78479  
Rhesus blood group antigen-like protein isoform VIII - human  
C/Species: Homo sapiens (man)  
C/Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 15-Jun-2001  
C/Accession: S78479; S26563

R/Collin, Y.  
submitted to the EMBL Data Library, November 1991  
A/Reference number: S78478  
A/Accession: S78479  
A/Molecule type: mRNA  
A/Residues: 1-266 <COL>  
A/Cross-references: EMBL:X63096; NID:936044; PIDN:CAA44810.1; PID:936045  
R/Le Van Kim, C.; Cherif-Zahar, B.; Raynal, V.; Mouru, I.; Lopez, M.; Carttron, J.P.; Coll Blood 80, 1074-1078, 1992  
A/Title: Multiple Rh messenger RNA isoforms are produced by alternative splicing.  
A/Reference number: S26560; MUID:92360855; PMID:1379850  
A/Accession: S26563  
A/Molecule type: mRNA  
A/Residues: 160-266 <LEV>  
A/Cross-references: EMBL:X63096  
A/Experimental source: tissue-type bone marrow  
C/Superfamily: human erythrocyte membrane protein Rhd  
C/Keywords: alternative splicing; erythrocyte; surface antigen; transmembrane protein

```

Query Match 51.3%; Score 1089.5; DB 2; Length 266;
Best Local Similarity 58.0%; Pred. No. 1.2e-79;
Matches 242; Conservative 3; Mismatches 21; Indels 151; Gaps 1;

QY 1 MSCKPSRYORCLPICALTLTEAALILFFFTTHDASLEDQGLVASVYOGDITVMAAI 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MSSKTPSVRCCLPLMALTEAALILFFFTTHDASLEDQGLVATYQVGDITVMAAI 60
QY 61 GIGFLTSPRRHSSWSVAENLFMLALGVOMAILLDGFLSQPPSGKVITLPSIMLATMSA 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 GIGFLTSPRRHSSWSVAENLFMLALGVOMAILLDGFLSQPPSGKVITLPSIRLATMSA 120
QY 121 LSVLISVDVAVLGKVNLAQLVWVVLVEVTDLGNIIRWVINSIFNTDYHMMNMHIYVFAAYFG 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 MSVLISAGAVLGKVNLAQLVWVVLVEVTDLGTLRWVINSIFNTDYHMMNRHYVFAAYFG 180
QY 181 LTVAMCLPKPLPEGTEDNDORATIPSLSAMLGALFLMFRPSVNSALIRSPIERKNAVEN 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LTVAMCLPKPLPEGTEDNDORATIPSLSAMLGALFLMFRPSVNSALIRSPIERKNAVEN 240
QY 241 TYVAVAVSVTVAISGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIVLGLV 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 TYVAVAVSVTVAISGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIVLGLV 300
QY 301 AGLISVRGAKYLP 313
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 AGLISIGAKCLP 313
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 164 -----CONRVLGTHHSVMSISFSLGILGELITVVLVLAHTVNGNGMTG 209
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 164 -----CONRVLGTHHSVMSISFSLGILGELITVVLVLAHTVNGNGMTG 209
QY 361 FQVLLSIGELSLAIVIALTSGILTLALLNLKIRAPHEAKYFDDQVFWKPHLAAGV 417
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 210 FQVLLSIGELSLAIVIALTSGILTLALLNLKIRAPHEAKYFDDQVFWKPHLAAGV 417
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 13  
S78478  
Rhesus blood group antigen-like protein isoform VI - human  
C/Species: Homo sapiens (man)  
C/Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 15-Jun-2001  
C/Accession: S78478; S26562  
R/Collin, Y.  
submitted to the EMBL Data Library, November 1991  
A/Reference number: S78478  
A/Accession: S78478  
A/Molecule type: mRNA  
A/Residues: 1-267 <COL>  
A/Cross-references: EMBL:X63095; NID:936042; PIDN:CAA44809.1; PID:936043  
R/Le Van Kim, C.; Cherif-Zahar, B.; Raynal, V.; Mouru, I.; Lopez, M.; Carttron, J.P.; Coll Blood 80, 1074-1078, 1992  
A/Title: Multiple Rh messenger RNA isoforms are produced by alternative splicing.  
A/Reference number: S26560; MUID:92360855; PMID:1379850  
A/Accession: S26562  
A/Molecule type: mRNA  
A/Residues: 160-267 <LEV>  
A/Cross-references: EMBL:X63095

A: Experimental source: tissue-type bone marrow  
C: Superfamily: human erythrocyte membrane protein Rhd  
E: Keywords: alternative splicing; erythrocyte; surface antigen; transmembrane protein

Query Match 47.1%; Score 1000.5; DB 2; Length 267;  
Best Local Similarity 61.5%; Pred. No. 1.5e-72;  
Matches 220; Conservative 7; Mismatches 26; Indels 105; Gaps 1;

```
QY 1 MSCKYPPSVRCPLCLLTLEALILFFFTTHYDASLEQKGLVASYQVGGDTLVMAAI 60
DB 1 MSSKYPSSVRRCPLMLTLEALILFFFTTHYDASLEQKGLVASYQVGGDTLVMAAL 60
QY 61 GLEFLTSPPRRHSSVAFLMLALGVQVAILLDGFLSQPPSGKVITLPSILATMSA 120
DB 61 GLEFLTSPPRRHSSVAFLMLALGVQVAILLDGFLSQPPSGKVITLPSILATMSA 120
QY 121 LSVLISVDAYLGVKNLAQLVVMVLEVTDLGNLMVLSNIFNTDYHMMMHIVFAA 180
DB 121 MSVLISGAVLGVKNLAQLVVMVLEVTALGTLRMVISNIFN----- 162
QY 181 LTVAMCLPKLPKEGTENDQRATIPSLAMLGALFLMFRPSVNSALLRSPIERKKA 240
DB 163 ----- 162
QY 241 TYAAVAASVVTATAGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIVL 300
DB 163 ----- 162
QY 163 ----- 162
DB 163 ----- 162
QY 301 AGHISVGAAYLPGCCNRVLGIPHSIMGVNFSILGLLEIITVLLVDTVGANGNM 358
DB 196 AGHISVGAAYLPGCCNRVLGIPHSIMGVNFSILGLLEIITVLLVDTVGANGNM 253
```

## RESULT 14

S29124  
membrane glycoprotein, 50K, erythrocyte - human  
C:Species: Homo sapiens (man)  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C/Accession: S29124, J08168  
R:Ridgwell, K.; Spurt, N.K.; Laguda, B.; MacGeoch, C.; Arent, N.D.; Tanner, M.J.A.  
Biochem. J. 287, 223-228, 1992  
A:Title: Isolation of cDNA clones for a 50 kDa glycoprotein of the human erythrocyte mem  
A:Reference number: S29124; MUID:93038558; PMID:1417776  
A:Accession: S29124  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-409 <RID>  
A:Cross-references: UNIPROT:Q02094; EMBL:X64594; NID:G31194; PIDN:CAA45883.1; PID:G31195  
R:Iwamoto, S.; Omi, T.; Yamashita, M.; Okuda, H.; Kawano, M.; Kajii, E.  
Biochem. Biophys. Res. Commun. 243, 233-240, 1998  
A:Title: Identification of 5' flanking sequence of RH50 gene and the core region for ery  
A:Reference number: J08168; MUID:98139897; PMID:9473510  
A:Accession: J08168  
A:Molecule type: mRNA  
A:Residues: 1-52 <IMA>  
C:Comment: This protein is membrane protein tightly associated with Rh polypeptides and  
C:Gene: RH50  
A:Superfamily: human erythrocyte membrane protein Rhd  
C:Keywords: glycoprotein; transmembrane protein

Query Match 25.8%; Score 547.5; DB 2; Length 409;  
Best Local Similarity 33.9%; Pred. No. 3.8e-36;  
Matches 139; Conservative 79; Mismatches 111; Indels 21; Gaps 7;  
QY 14 PLCLATLEALILFFFTTHY--DASLEQKGLVASYQV-----ODLVMAAIGL 62  
DB 6 PLMAIVLEIMIVLFGFVEYEDQVTLQDNLITKPRDMGIFPELVLPQDVMMIFGVF 65  
QY 63 GFLTSPPRRHSSVAFLMLALGVQVAILLDGFLSQPPSGKVITLPSILATMSA 122  
DB 66 GFLMTLPKRYGFSVGINLVLAALGLQWGTIVGIL--QSGQKFNIGIKMIMNADFSAA 124

```
QY 123 VLSVDAYLGVKNLAQLVVMVLEVTDLGNLMVLSNIFNTDYHMMMHIVFAA 182
DB 125 VLSVFGAVLGVKNLAQLVVMVLEVTALGTLRMVISNIFN----- 162
QY 183 VAMCLPKLPKEGTENDQRATIPSLAMLGALFLMFRPSVNSALLRSPIERKKA 242
DB 185 VAGILVRSGLRKHEBESAYSDLFAMIGTLPMLFMFSPFNALBPQKQCRATVDY 244
QY 243 YAAVAVSVTATAGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIVL 302
DB 245 FSLAACVLTAFAPSSVLEHKGKLMVHIONATLGGVAVAGTCADMAIHFGSMI 304
QY 303 LISVGAAYLPGCCNRVLGIPHSIMGVNFSILGLLEIITVLLVDTVGANGNM 361
DB 305 MSVLISGAVLGVKNLAQLVVMVLEVTALGTLRMVISNIFN----- 162
QY 362 QVLSIGELSLAIVALTSGLTALLNLKIRKAPRPAKYPDDQVFWKRP 411
DB 361 QA-----ALGSSIGTAVGGLMTGLTKLPRLMGQPSDQNCYDSSVYWKVP 406
```

## RESULT 15

T29442  
hypothetical protein F08F3.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T29442  
R:Blanchard, M.; Bradshaw, H.  
submitted to the EMBL Data Library, July 1996  
A:Description: The sequence of C. elegans cosmid F08F3.  
A:Reference number: Z20620  
A:Accession: T29442  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-463 <BLA>  
A:Cross-references: UNIPROT:Q22947; EMBL:U64847; PIDN:AB04874.1; GSPDB:GN00023; CESP:F08  
A:Experimental source: strain Bristol N2; clone F08F3  
C:Gene: F08F3.3  
A:Map position: 5  
A:Intons: 18/3; 167/3; 266/2; 442/3  
C:Superfamily: human erythrocyte membrane protein Rhd

Query Match 19.4%; Score 412; DB 2; Length 463;  
Best Local Similarity 26.6%; Pred. No. 2.9e-25;  
Matches 116; Conservative 88; Mismatches 190; Indels 42; Gaps 8;

```
QY 10 QRCPLCALTLLEALILFFFTTHYDAS-----LEQKGLVASYQVGGDTLVMAAIG 61
DB 7 QNQLTILGLFQVPLVLPALYSYDASLPSETKVEBAKMTNLYPLFQDTHWIFIG 66
QY 62 LGEFLTSPPRRHSSVAFLMLALGVQVAILLDGFLSQPPSGKVITLPSILATMSA 121
DB 67 FGEFLMTLPKRYGFSVGINLVLAALGLQWGTIVGIL--QSGQKFNIGIKMIMNADFSAA 126
QY 122 VLSVDAYLGVKNLAQLVVMVLEVTDLGNLMVLSNIFNTDYHNM-----MHIVFAA 177
DB 127 VLSISGAVLGVKNLAQLVVMVLEVTALGTLRMVISNIFN----- 162
QY 178 YFGLTVAWCLPKLPKEGTENDQRATIPSLAMLGALFLMFRPSVNSALLRSPIERKKA 237
DB 183 YFGLTVAWCLPKLPKEGTENDQRATIPSLAMLGALFLMFRPSVNSALLRSPIERKKA 237
QY 238 VENTYAAVAVSVTATAGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIVL 302
DB 242 VANTFSLACACTWTFTPLVQADVKKRPFMVHIANSTLAGVAIGTTAVVLPYHAMIT 301
QY 298 GLVAGLISVGAAYLPGCCNRVLGIPHSIMGVNFSILGLLEIITVLLV----- 349
DB 302 GVLVAGVAVIYGYITLTPSEKLGINDGVNNLHMPGLIAGFASIAFPTIDETRYPA 361
QY 350 --DTV--GANG-----MIGFVLSIGELSLAIVALTSGLTALLNLKIRKA 395
```

Db	362	OYDKIYPMARGEDRTMFEDEKTOALNOJMAIGVFLASTV---	SGYLTGILLKUKIWDQ	418
Oy	396	PHEAKYFDDQVFWKPP		411
		: :   :   : :		
Db	419	VRDEYVADGDYFETP		434

Search completed: March 24, 2005, 13:17:05  
Job time : 22 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model1

Run on: March 24, 2005, 13:13:48 ; Search time 68 Seconds  
(without alignments)  
3140.250 Million cell updates/sec

Title: CAC07879  
Perfect score: 2124  
Sequence: 1 MSCKYRSVGRCLPLCALTL.....EAKYFDQVFWKPEHLAVGF 417

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1986	93.5	417	2	Q6KC49
2	1981	93.3	417	2	Q81ZT1
3	1980	93.2	417	2	Q7RU08
4	1978	93.1	417	2	Q6SV89
5	1977	93.0	417	2	Q6A1H2
6	1975	93.0	416	1	RHD_HUMAN
7	1975	93.0	417	2	Q9UK19
8	1974	92.9	417	2	Q6A1H3
9	1972	92.8	417	2	Q6A1H4
10	1972	92.8	417	2	Q9NXX8
11	1971	92.8	417	2	Q6SV88
12	1970	92.7	417	2	Q81ZT0
13	1970	92.7	417	2	Q6SV90
14	1969	92.7	417	2	Q6SV87
15	1969	92.7	417	2	Q6SV91
16	1967	92.6	417	2	Q70HW2
17	1964.5	92.5	416	2	Q6A1H1
18	1961	92.3	417	2	Q99906
19	1957	92.1	417	2	Q9CA07
20	1951	91.9	417	2	Q9HCC3
21	1942	91.4	417	2	Q9H2A8
22	1932	91.0	417	2	Q9UD25
23	1897	89.3	417	2	Q9UK74
24	1896	89.3	417	2	Q7ZS94
25	1866	87.9	417	2	Q81ZT5
26	1862	87.7	417	2	Q9UPN0
27	1859	87.5	417	2	Q6AZX5
28	1858	87.5	416	1	RHLR_PANTR
29	1855	87.3	417	2	Q81ZT3
30	1855	87.3	417	2	Q6J2U3
31	1849	87.1	417	2	Q7RU06

32	1845	86.9	417	2	Q81ZT4	Q81ZC4 homo sapien
33	1838	86.5	417	2	Q81ZT2	Q81ZC2 homo sapien
34	1837	86.5	416	1	RHLD_GORGO	Q284T7 gorilla gor
35	1835	86.4	416	1	RHLA_PANTR	Q284T3 pan troglod
36	1828	86.1	416	1	RHCF_HUMAN	P185T7 homo sapien
37	1806	85.0	416	1	RHLF_PANTR	Q284T2 pan troglod
38	1798	84.7	416	1	RHLC_GORGO	Q284T6 gorilla gor
39	1605	75.6	401	2	Q6ZSC4	Q6Z6C4 homo sapien
40	1526	71.8	407	2	Q975Z5	Q975Z5 pongo pygma
41	1519	71.5	416	1	RHL_MACMU	Q284T1 macaca mulla
42	1504	70.8	416	1	RHL_MACFA	Q284T1 macaca fasc
43	1493	70.3	398	2	Q9UP91	Q9UP91 homo sapien
44	1448	68.2	407	2	Q979S8	Q979S8 papio hamad
45	1412	66.5	405	2	Q9TTF4	Q9TTF4 cebus apell

ALIGNMENTS

RESULT 1	ID	Q6KC49	PRELIMINARY;	PRT;	417 AA.
AC	Q6KC49				
DT	05-JUL-2004	(TrEMBLrel. 27, Created)			
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)			
DE	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)			
DE	Rhesus blood group D antigen (Fragment).				
GN	Name=RHD;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Peripheral blood;				
RX	MEDLINE=93320449; PubMed=8329718;				
RA	Arce M.A., Thompson E.S., Wagner S., Coyne K.E., Ferdman B.A.,				
RA	Lablitz D.M.;				
RT	"Molecular cloning of Rhd cDNA derived from a gene present in Rhd-				
RT	positive, but not Rhd-negative individuals.";				
RL	Blood 82:651-655(1993).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Peripheral blood;				
RA	Doeschner A., Petershofen E.K., Schunter F., Wagner F.;				
RT	"New RHD alleles with previously unknown polymorphism.";				
RL	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AJ704215; CAG284848.2; -.				
DR	GO; GO:0016020; C:membrane; IEA.				
DR	InterPro; IPR002229; RhesusRHD.				
DR	InterPro; IPR010256; RH_like_transp.				
DR	Pfam; PF00909; Ammonium_transp; 1.				
FT	PRINTS; PR00342; RHEUSRHD.				
FT	NON_TER 417				
SQ	SEQUENCE 417 AA; 45124 MW; CEE643297E036559 CRC64;				
Query Match	93.5%;	Score 1986;	DB 2;	Length 417;	
Best Local Similarity	95.2%;	Pred. No. 3.9e-135;			
Matches 397;	Conservative	4;	Mismatches 16;	Indels 0;	Gaps 0;
QY	1	MSCKYRSVORCPCLCALTLLEALILLFYFTHYDASLEDOKGLVASVYQGDLTWAAI	60		
DB	1	MSCKYRSVGRCLPLNAVTLEALLILFFFTHYDASLEOKGLVASVYQGDLTWAAI	60		
QY	61	GLGFLTSSFRHSSVAFNLFMIALGVQVAIILLDGFLSQPSGKVVITLFSIWLATWSA	120		
DB	61	GLGFLTSSFRHSSVAFNLFMIALGVQVAIILLDGFLSQPSGKVVITLFSIWLATWSA	120		
QY	121	LSVLISVDALGVNLAQLVVMTLVEVTDLGNRMVYSNIFNDDYHNNMMHIVFAAYFG	180		
DB	121	LSVLISVDALGVNLAQLVVMTLVEVTALGNRMVYSNIFNDDYHNNMMHIVFAAYFG	180		
QY	181	LTVAMCLPKPLPCTEDNDQRAITPISLAMLGALFLMMPRPVSALLRSPERKNAVEN	240		

```
Db 181 LSVAMCPLPKECTEDKQATIPSLSAMGLFLMFWPSPNSALLSPERKNAVN 240
Qy 241 TYAAVAASVVTATISGSSLAHPQCKISTYGHSAVLPEGVAVDTSCHLIPSPMLPIVLGLV 300
Db 241 TYAAVAASVVTATISGSSLAHPQCKISTYGHSAVLPEGVAVDTSCHLIPSPMLPIVLGLV 300
Qy 301 AGLISVGAKYLPGCCNRVLGIPHSSIMGNFSLGLLEIYIYVLVDTVGANGMTG 360
Db 301 AGLISVGAKYLPGCCNRVLGIPHSSIMGNFSLGLLEIYIYVLVDTVGANGMTG 360
Qy 361 FOVLISIGELSLAIVIALTSGLLTALLNLIKIRKAPHEAKYFDDQYFWKPHLAVGF 417
Db 361 FOVLISIGELSLAIVIALTSGLLTALLNLIKIRKAPHEAKYFDDQYFWKPHLAVGF 417
```

## RESULT 2

```
081ZT1 PRELIMINARY; PRT; 417 AA.
ID 081ZT1
AC 081ZT1
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DE Rheus blood group D antigen D(667) variant.
OS Homo sapiens (Human).
OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22320945; PubMed=1293640; DOI=10.1182/blood-2002-01-0229;
RA Noizat-Pirenne F., Lee K., Le Pennec P.Y., Simon P., Kazup P.,
RA Roucher D., Kozraud A.M., Rousset M., Juszczak G., Menanteau C.,
RT "Rare RHCE phenotypes in black individuals of Afro-Caribbean origin:
RT identification and transfusion safety."
RL Blood 100:4223-4231(2002)
RL EMBL; AF510069; AAN75125.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR011058; Cytochrome-N.
DR InterPro; IPR002229; RhesusRHD.
DR Pfam; PF00909; RHL like transp.
DR PRINTS; PR00342; RhesusRHD.
SQ SEQUENCE 417 AA; 4514 MW; C65D3A1ED5DAD87 CRC64;
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Query Match 93.3%; Score 1981; DB 2; Length 417;  
Best Local Similarity 95.2%; Pred. No. 9e-135;  
Matches 397; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

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Qy 1 MSCKYPRSVORCLPLCALTLLEAAILLFYFTHYDASLEDDQGLVASVYQGDITVMAAI 60
Db 1 MSCKYPRSVORCLPLCALTLLEAAILLFYFTHYDASLEDDQGLVASVYQGDITVMAAI 60
Qy 61 GLGFLTSSFRHSSWSVAFLFMLALGVQWAILLDGFLSQPSPSKVITLFSIRLATMSA 120
Db 61 GLGFLTSSFRHSSWSVAFLFMLALGVQWAILLDGFLSQPSPSKVITLFSIRLATMSA 120
Qy 121 LSVLISVDAVIGKVNLAQLVVMVLEVTDLGNLRLVTSNIFNTDYNHMMHIVYFAAYFG 180
Db 121 LSVLISVDAVIGKVNLAQLVVMVLEVTDLGNLRLVTSNIFNTDYNHMMHIVYFAAYFG 180
Qy 181 LTVAMCPLPKECTEDKQATIPSLSAMGLFLMFWPSPNSALLSPERKNAVN 240
Db 181 LTVAMCPLPKECTEDKQATIPSLSAMGLFLMFWPSPNSALLSPERKNAVN 240
Qy 241 TYAAVAASVVTATISGSSLAHPQCKISTYGHSAVLPEGVAVDTSCHLIPSPMLPIVLGLV 300
Db 241 TYAAVAASVVTATISGSSLAHPQCKISTYGHSAVLPEGVAVDTSCHLIPSPMLPIVLGLV 300
Qy 301 AGLISVGAKYLPGCCNRVLGIPHSSIMGNFSLGLLEIYIYVLVDTVGANGMTG 360
Db 301 AGLISVGAKYLPGCCNRVLGIPHSSIMGNFSLGLLEIYIYVLVDTVGANGMTG 360
```

```
Qy 361 FOVLISIGELSLAIVIALTSGLLTALLNLIKIRKAPHEAKYFDDQYFWKPHLAVGF 417
Db 361 FOVLISIGELSLAIVIALTSGLLTALLNLIKIRKAPHEAKYFDDQYFWKPHLAVGF 417
```

## RESULT 3

```
Q7RU08 PRELIMINARY; PRT; 417 AA.
ID Q7RU08
AC Q7RU08
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DE Rheus blood group D antigen D(667) variant.
OS Homo sapiens (Human).
OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21898876; PubMed=11902138; DOI=10.1182/blood-2001-12-0153;
RA Wagner F.F., Flegel W.A.;
RT "RHCE represents the ancestral RH position, while RHD is the
RT duplicated gene."
RL Blood 99:2272-2273(2002).
CC -1- MISCLEBANBUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BN000065; CAD29848.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR011058; Cytochrome-N.
DR InterPro; IPR002229; RhesusRHD.
DR Pfam; PF00909; RHL like transp.
DR PRINTS; PR00342; RhesusRHD.
SQ SEQUENCE 417 AA; 45180 MW; 649F1BFA664AE7DB CRC64;
```

Query Match 93.2%; Score 1980; DB 2; Length 417;  
Best Local Similarity 95.2%; Pred. No. 1.1e-134;  
Matches 397; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

```
Qy 1 MSCKYPRSVORCLPLCALTLLEAAILLFYFTHYDASLEDDQGLVASVYQGDITVMAAI 60
Db 1 MSCKYPRSVORCLPLCALTLLEAAILLFYFTHYDASLEDDQGLVASVYQGDITVMAAI 60
Qy 61 GLGFLTSSFRHSSWSVAFLFMLALGVQWAILLDGFLSQPSPSKVITLFSIRLATMSA 120
Db 61 GLGFLTSSFRHSSWSVAFLFMLALGVQWAILLDGFLSQPSPSKVITLFSIRLATMSA 120
Qy 121 LSVLISVDAVIGKVNLAQLVVMVLEVTDLGNLRLVTSNIFNTDYNHMMHIVYFAAYFG 180
Db 121 LSVLISVDAVIGKVNLAQLVVMVLEVTDLGNLRLVTSNIFNTDYNHMMHIVYFAAYFG 180
Qy 181 LTVAMCPLPKECTEDKQATIPSLSAMGLFLMFWPSPNSALLSPERKNAVN 240
Db 181 LTVAMCPLPKECTEDKQATIPSLSAMGLFLMFWPSPNSALLSPERKNAVN 240
Qy 241 TYAAVAASVVTATISGSSLAHPQCKISTYGHSAVLPEGVAVDTSCHLIPSPMLPIVLGLV 300
Db 241 TYAAVAASVVTATISGSSLAHPQCKISTYGHSAVLPEGVAVDTSCHLIPSPMLPIVLGLV 300
Qy 301 AGLISVGAKYLPGCCNRVLGIPHSSIMGNFSLGLLEIYIYVLVDTVGANGMTG 360
Db 301 AGLISVGAKYLPGCCNRVLGIPHSSIMGNFSLGLLEIYIYVLVDTVGANGMTG 360
```

## RESULT 4

```
Q6SV89 PRELIMINARY; PRT; 417 AA.
```

```

AC Q68V89;
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Rhesus blood group D antigen DLA (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Noizat-Pirenne F., Ansart-Pirenne H.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY449383; AAR24080.1;
DR GO: GO:0016020; C:membrane; IEA.
DR InterPro: IPR011058; Cytochrome-N.
DR InterPro: IPR010256; RH like transp.
DR Pfam: PF00909; Ammonium transp; 1.
DR PRINTS: PR00342; RHEUSRD.
FT NON_TER 417
SQ SEQUENCE 417 AA; 45261 MW; C9E27FE4A9EE2DD CRC64;

Query Match 93.1%; Score 1978; DB 2; Length 417;
Best Local Similarity 95.0%; Pred. No. 1.5e-134;
Matches 396; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 MSCKPRSVQRCLPLCALTEALILLFYFTTHYDASLEDOKGLVASVQVGDITVMAI 60
DB 1 MSCKPRSVQRCLPLMALTEALILLFYFTTHYDASLEDOKGLVASVQVGDITVMAI 60
QY 61 GLGFLTSSFRHSSSVAFNLFMLALGVQWAILDGLFSQPPSGKVITLFSITLWMSA 120
DB 61 GLGFLTSSFRHSSSVAFNLFMLALGVQWAILDGLFSQPPSGKVITLFSITLWMSA 120
QY 121 LSVLISYDAVLGKYNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNHIYVFAAYFG 180
DB 121 LSVLISYDAVLGKYNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNHIYVFAAYFG 180
QY 121 LSVLISYDAVLGKYNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNHIYVFAAYFG 180
DB 121 LSVLISYDAVLGKYNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNHIYVFAAYFG 180
QY 181 LTVAMCPLKPLPEGTEDNDQATIPSLSAMGALFLMFPSPVNSALLRSPIERKNAVFN 240
DB 181 LTVAMCPLKPLPEGTEDNDQATIPSLSAMGALFLMFPSPVNSALLRSPIERKNAVFN 240
QY 181 LTVAMCPLKPLPEGTEDNDQATIPSLSAMGALFLMFPSPVNSALLRSPIERKNAVFN 240
DB 181 LTVAMCPLKPLPEGTEDNDQATIPSLSAMGALFLMFPSPVNSALLRSPIERKNAVFN 240
QY 241 TYVAVASVVTALISGSSLAHPQKISKTYGHSVLPESVAVDTSCHLIPSPMLPIVGLV 300
DB 241 TYVAVASVVTALISGSSLAHPQKISKTYGHSVLPESVAVDTSCHLIPSPMLPIVGLV 300
QY 241 TYVAVASVVTALISGSSLAHPQKISKTYGHSVLPESVAVDTSCHLIPSPMLPIVGLV 300
DB 241 TYVAVASVVTALISGSSLAHPQKISKTYGHSVLPESVAVDTSCHLIPSPMLPIVGLV 300
QY 301 AGLISVGAKYLPCCNCRVLGIPHSITGYNFSLGLEEIIYVLVLDTVGANGMIG 360
DB 301 AGLISVGAKYLPCCNCRVLGIPHSITGYNFSLGLEEIIYVLVLDTVGANGMIG 360
QY 361 FOVLISIGELSLAIVIALTSGLTGLTLNLKIMKAPHEAKYFDQVFWKPHLAVGF 417
DB 361 FOVLISIGELSLAIVIALTSGLTGLTLNLKIMKAPHEAKYFDQVFWKPHLAVGF 417

RESULT 5
ID 06A1H2 PRELIMINARY; PRT; 417 AA.
AC 06A1H2;
DT 25-OCT-2004 (TREMblrel. 28, Created)
DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
DE Rhesus blood group D antigen (Fragment).
GN Name=RHD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Peripheral blood;
RC Doescher A., Wagner F., Schunter F., Peterhofen E.K.;

```

```

RT "Four new RHD alleles with previously unknown polymorphism.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ784311; CAH04921.1;
DR GO: GO:0016020; C:membrane; IEA.
DR InterPro: IPR011058; Cytochrome-N.
DR InterPro: IPR002229; RhesusRD.
DR InterPro: IPR010256; RH like transp.
DR Pfam: PF00909; Ammonium transp; 1.
DR PRINTS: PR00342; RHEUSRD.
FT NON_TER 417
SQ SEQUENCE 417 AA; 45212 MW; 649F1BF364AF7D0 CRC64;

Query Match 93.1%; Score 1977; DB 2; Length 417;
Best Local Similarity 95.0%; Pred. No. 1.8e-134;
Matches 396; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 MSCKPRSVQRCLPLCALTEALILLFYFTTHYDASLEDOKGLVASVQVGDITVMAI 60
DB 1 MSCKPRSVQRCLPLMALTEALILLFYFTTHYDASLEDOKGLVASVQVGDITVMAI 60
QY 61 GLGFLTSSFRHSSSVAFNLFMLALGVQWAILDGLFSQPPSGKVITLFSITLWMSA 120
DB 61 GLGFLTSSFRHSSSVAFNLFMLALGVQWAILDGLFSQPPSGKVITLFSITLWMSA 120
QY 121 LSVLISYDAVLGKYNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNHIYVFAAYFG 180
DB 121 LSVLISYDAVLGKYNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNHIYVFAAYFG 180
QY 121 LSVLISYDAVLGKYNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNHIYVFAAYFG 180
DB 121 LSVLISYDAVLGKYNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNHIYVFAAYFG 180
QY 181 LTVAMCPLKPLPEGTEDNDQATIPSLSAMGALFLMFPSPVNSALLRSPIERKNAVFN 240
DB 181 LTVAMCPLKPLPEGTEDNDQATIPSLSAMGALFLMFPSPVNSALLRSPIERKNAVFN 240
QY 181 LTVAMCPLKPLPEGTEDNDQATIPSLSAMGALFLMFPSPVNSALLRSPIERKNAVFN 240
DB 181 LTVAMCPLKPLPEGTEDNDQATIPSLSAMGALFLMFPSPVNSALLRSPIERKNAVFN 240
QY 241 TYVAVASVVTALISGSSLAHPQKISKTYGHSVLPESVAVDTSCHLIPSPMLPIVGLV 300
DB 241 TYVAVASVVTALISGSSLAHPQKISKTYGHSVLPESVAVDTSCHLIPSPMLPIVGLV 300
QY 241 TYVAVASVVTALISGSSLAHPQKISKTYGHSVLPESVAVDTSCHLIPSPMLPIVGLV 300
DB 241 TYVAVASVVTALISGSSLAHPQKISKTYGHSVLPESVAVDTSCHLIPSPMLPIVGLV 300
QY 301 AGLISVGAKYLPCCNCRVLGIPHSITGYNFSLGLEEIIYVLVLDTVGANGMIG 360
DB 301 AGLISVGAKYLPCCNCRVLGIPHSITGYNFSLGLEEIIYVLVLDTVGANGMIG 360
QY 361 FOVLISIGELSLAIVIALTSGLTGLTLNLKIMKAPHEAKYFDQVFWKPHLAVGF 417
DB 361 FOVLISIGELSLAIVIALTSGLTGLTLNLKIMKAPHEAKYFDQVFWKPHLAVGF 417

RESULT 6
ID RHD_HUMAN STANDARD; PRT; 416 AA.
AC Q02161; Q02162; Q07618; Q16147; Q16235; Q16355; Q9NPK0; Q9NQ02;
AC Q9NQ02; Q9NQ02; Q9NQ23;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Blood group Rh(D) polypeptide (Rhesus D antigen) (RHXIII) (Rh
DE polypeptide 2) (RhDII).
GN Name=RHD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Bone marrow;
RC MEDLINE=9306356; PubMed=1438298;
RX le van Kim C., Mouru I., Cherif-Zahar B., Raynal V., Chertier C.,
RA Cartoon J.-P., Colin Y.;
RT "Molecular cloning and primary structure of the human blood group Rhd
RT polypeptide.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10925-10929 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RA Tissue=Bone marrow;
RC

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RX MEDLINE=92360855; PubMed=1379850;  
 RA le van Kim C., Cherif-Zahar B., Raynal V., Mouro I., Lopez M.,  
 RA Cartton J.-P., Colin Y.;  
 RT "Multiple Rh messenger RNA isoforms are produced by alternative  
 RT splicing.";  
 RL Blood 80:1074-1078 (1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=93320449; PubMed=8329718;  
 RA Arce M.A., Thompson E.S., Wagner S., Coyne K.E., Ferdman B.A.,  
 RA Lublin D.M.;  
 RA "Molecular cloning of Rhd cDNA derived from a gene present in Rhd-  
 RT positive, but not Rhd-negative individuals.";  
 RL Blood 82:651-655 (1993).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=933216282; PubMed=7916743;  
 RA Kajii E., Umenishi F., Iwamoto S., Ikemoto S.;  
 RA "Isolation of a new cDNA clone encoding an Rh polypeptide associated  
 RT with the Rh blood group system.";  
 RL Hum. Genet. 91:157-162 (1993).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=95329738; PubMed=7606008;  
 RA Huang C.-H., Reid M.E., Chen Y.;  
 RA "Identification of a partial internal deletion in the RH locus causing  
 RT the human erythrocyte D-phenotype.";  
 RL Blood 86:784-790 (1995).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RA MEDLINE=94235883; PubMed=8180407;  
 RA Westhoff C.M., Wylie D.E.;  
 RA "Identification of a new Rhd-specific mRNA from K562 cells.";  
 RL Blood 83:3098-3100 (1994).  
 RN [7]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RA MEDLINE=94362249; PubMed=8080999;  
 RA Suyama K., Lum R., Haller S., Goldstein J.;  
 RA "Rh(D) antigen expression and isolation of a new Rh(D) cDNA isoform in  
 RT human erythroleukemic K562 cells.";  
 RL Blood 84:1975-1981 (1994).  
 RN [8]  
 RP SEQUENCE FROM N.A., AND VARIANTS VAL-222; GLN-232; MET-237 AND  
 RP LEU-244.  
 RA Hyodo H., Ishikawa Y., Kashiwase K., Ogawa A., Matnabe Y.,  
 RA Tsuneyama H., Toyoda C., Uchikawa M., Akaza T., Fujii T.;  
 RA "Polymorphisms of RHDVA in Japanese.";  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RN [9]  
 RP VARIANT BLOOD GROUP TAR.  
 RA MEDLINE=95259709; PubMed=7741145;  
 RA Rouillac C., le van Kim C., Beolet M., Cartton J.-P., Colin Y.;  
 RA "Leu10PcO substitution in the Rhd polypeptide is responsible for the  
 RT DVI category blood group phenotype.";  
 RL Am. J. Hematol. 49:87-88 (1995).  
 CC -1- FUNCTION: May be part of an oligomeric complex which is likely to  
 CC have a transport or channel function in the erythrocyte membrane.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1; Synonyms=long;  
 CC IsoId=002161-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Short 1;  
 CC IsoId=002161-2; Sequence=VSP\_005706;  
 CC Name=3; Synonyms=Short 2;  
 CC IsoId=002161-3; Sequence=VSP\_005707, VSP\_005708;  
 CC -1- TISSUE SPECIFICITY: Restricted to tissues or cell lines expressing  
 CC erythroid characters.  
 CC -1- POLYMORPHISM: RHD and RHCE are responsible for the Rh blood group  
 CC system. The molecular basis of the Tar=Rh40 blood group antigen is  
 CC a polymorphism in position 109.  
 CC -1- SIMILARITY: Belongs to the Rh family.  
 CC -----

CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.ebi.ac.uk/announcements">http://www.ebi.ac.uk/announcements</a> or send an email to <a href="mailto:license@ebi.ac.uk">license@ebi.ac.uk</a> ).			
CC	-----			
DR	EMBL	X63097	CMA44811.1	-
DR	EMBL	X63094	CMA44808.1	-
DR	EMBL	L08429	AAA02679.1	-
DR	EMBL	S57971	AAA26081.1	-
DR	EMBL	S78509	AAA34852.1	-
DR	EMBL	S70174	AAA30756.1	-
DR	EMBL	S73913	AAA31911.1	-
DR	EMBL	AB018966	BAA81899.1	-
DR	EMBL	AB018967	BAA81900.1	-
DR	EMBL	AB018968	BAA81901.1	-
DR	EMBL	AB018969	BAA82159.1	-
DR	PIR	A46368	A46368	-
DR	PIR	I52615	I52615	-
DR	Genew	HCNC:10009	RHD	-
DR	MIM	111680	-	-
DR	GO	GO:0005887	C:integral to plasma membrane; TAS	-
DR	InterPro	IPR01058	Cyanovirin-N	-
DR	InterPro	IPR010256	RH like transp.	-
DR	InterPro	IPR002229	RhesusRHD	-
DR	Pfam	PF00909	Ammonium transp; 1	-
DR	PRINTS	PRO0342	RHESUSRHD	-
KM	Alternative splicing; Blood group antigen; Erythrocyte; Polymorphism; Transmembrane.			
KM	INIT_MET	0	0	-
FT	TRANSMEM	11	31	Potential.
FT	TRANSMEM	43	63	Potential.
FT	TRANSMEM	76	96	Potential.
FT	TRANSMEM	106	126	Potential.
FT	TRANSMEM	129	149	Potential.
FT	TRANSMEM	166	186	Potential.
FT	TRANSMEM	202	222	Potential.
FT	TRANSMEM	237	257	Potential.
FT	TRANSMEM	286	306	Potential.
FT	TRANSMEM	333	353	Potential.
FT	TRANSMEM	357	377	Potential.
FT	VASPLIC	313	408	Missing (in isoform 2).
FT	VASPLIC	315	315	/FTId=VSP_005706.
FT	VASPLIC	315	315	C -> S (in isoform 3).
FT	VASPLIC	316	416	/FTId=VSP_005707.
FT	VARIANT	109	109	Missing (in isoform 3).
FT	VARIANT	109	109	/FTId=VSP_005708.
FT	VARIANT	217	217	L -> P (in Tar antigen).
FT	VARIANT	217	217	/FTId=VAR_006919.
FT	VARIANT	217	217	M -> I.
FT	VARIANT	222	222	/FTId=VAR_006920.
FT	VARIANT	222	222	F -> V (in RhDva (FK) and RhDva (TT)).
FT	VARIANT	222	222	/FTId=VAR_013304.
FT	VARIANT	222	222	E -> Q (in RhDva (FK), RhDva (TO), RhDva (TT) and RhDvo).
FT	VARIANT	232	232	/FTId=VAR_013305.
FT	VARIANT	232	232	V -> M (in RhDva (TO) and RhDva (TT)).
FT	VARIANT	237	237	/FTId=VAR_013306.
FT	VARIANT	237	237	V -> L (in RhDva (TT)).
FT	VARIANT	244	244	/FTId=VAR_013307.
FT	VARIANT	244	244	W -> C (in Ref. 5).
FT	VARIANT	244	244	E -> G (in Ref. 4).
FT	VARIANT	244	244	S -> P (in Ref. 4).
FT	VARIANT	244	244	V -> A (in Ref. 4).
FT	VARIANT	244	244	V -> M (in Ref. 5).
FT	VARIANT	244	244	S -> T (in Ref. 4).
FT	VARIANT	244	244	G -> V (in Ref. 4).
FT	VARIANT	244	244	P -> H (in Ref. 4).
FT	VARIANT	244	244	E -> V (in Ref. 5).
FT	VARIANT	244	244	9136DFIA37D76B1B CRC64;
FT	VARIANT	244	244	SEQUENCE



Query Match 93.0%; Score 1975; DB 1; Length 416;  
Best Local Similarity 95.2%; Pred. No. 2.4e-134;  
Matches 396; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

QY 2 SCKYPSVORCLPLCALTEALILFFFTHYDASLEDOKGLVASYQVGODLTWMAIG 61  
DB 1 SSKYPSVRRCPLMALTEALILFFFTHYDASLEDOKGLVASYQVGODLTWMAIG 60  
QY 62 LGFLTSSFRHSHSSVAFNLFMLALGVQWAILLDGFLSOPPSGKVITLFSILATMSA 121  
DB 61 LGFLTSSFRHSHSSVAFNLFMLALGVQWAILLDGFLSOPPSGKVITLFSILATMSA 120  
QY 122 SVLISVDVAVGKVNLAQLVVWVLVEVTDLGNLRVINSINFTDYHNMNMHIYFAAYFG 181  
DB 121 SVLISVDVAVGKVNLAQLVVWVLVEVTDLGNLRVINSINFTDYHNMNMHIYFAAYFG 180  
QY 182 TVAMCLPKPLPEGTEDNDORATIPSLAMLGALFLMFRPSVNSALLRSPIERKNAVEN 241  
DB 181 SVAMCLPKPLPEGTEDNDORATIPSLAMLGALFLMFRPSVNSALLRSPIERKNAVEN 240  
QY 242 YYAAVAVSVTAISGSSLAHPQKISKTYGSAVLPEGVAVDTSCHLIPSPMLAVGLVA 301  
DB 241 YYAAVAVSVTAISGSSLAHPQKISKTYGSAVLPEGVAVDTSCHLIPSPMLAVGLVA 300  
QY 302 GLISVVGAKYLPGCCNRVLGIPHSSIMGYNFSLLGLEEIIYIVLVLDTVGAGNGMIG 361  
DB 301 GLISVVGAKYLPGCCNRVLGIPHSSIMGYNFSLLGLEEIIYIVLVLDTVGAGNGMIG 360

RESULT 7  
Q9UK19 PRELIMINARY; PRT; 417 AA.  
ID Q9UK19  
AC Q9UK19  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-MAY-2004 (TReMBLrel. 26, Last annotation update)  
DE Rhd type Iiia protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97398395; PubMed=9256293;  
RA Huang C.H., Chen Y., Reid M.;  
RT "Human Dylita) erythrocytes: Rhd protein is associated with multiple  
RT dispersed amino acid variations";  
RL Am. J. Hematol. 55:139-145(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Huang C.H.;  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF187846; AF04565.1; -.  
DR PIR; I54193;  
DR GO; GO:0016020; C:membrane; IEA.  
DR InterPro; IPR011058; Cytochrome-N.  
DR InterPro; IPR002229; RhesusRD.  
DR InterPro; IPR010256; RH\_like\_transp.  
DR Pfam; PF00909; Ammonium\_transp; I.  
DR PRINTS; PR00342; RHEUSRD.  
SQ SEQUENCE 417 AA; 45273 MW; 491FBI8A37957 CRC64;

Query Match 93.0%; Score 1975; DB 2; Length 417;  
Best Local Similarity 95.0%; Pred. No. 2.4e-134;  
Matches 396; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 MSCKYPSVORCLPLCALTEALILFFFTHYDASLEDOKGLVASYQVGODLTWMAI 60  
DB 1 MSCKYPSVORCLPLMALTEALILFFFTHYDASLEDOKGLVASYQVGODLTWMAI 60

QY 61 GLGFLTSSFRHSHSSVAFNLFMLALGVQWAILLDGFLSOPPSGKVITLFSILATMSA 120  
DB 61 GLGFLTSSFRHSHSSVAFNLFMLALGVQWAILLDGFLSOPPSGKVITLFSILATMSA 120  
QY 121 LSVLISVDVAVGKVNLAQLVVWVLVEVTDLGNLRVINSINFTDYHNMNMHIYFAAYFG 180  
DB 121 LSVLISVDVAVGKVNLAQLVVWVLVEVTDLGNLRVINSINFTDYHNMNMHIYFAAYFG 180  
QY 181 LTVAMCLPKPLPEGTEDNDORATIPSLAMLGALFLMFRPSVNSALLRSPIERKNAVEN 240  
DB 181 LTVAMCLPKPLPEGTEDNDORATIPSLAMLGALFLMFRPSVNSALLRSPIERKNAVEN 240  
QY 241 YYAAVAVSVTAISGSSLAHPQKISKTYGSAVLPEGVAVDTSCHLIPSPMLAVGLVA 300  
DB 241 YYAAVAVSVTAISGSSLAHPQKISKTYGSAVLPEGVAVDTSCHLIPSPMLAVGLVA 300  
QY 301 AGLSVVGAKYLPGCCNRVLGIPHSSIMGYNFSLLGLEEIIYIVLVLDTVGAGNGMIG 360  
DB 301 AGLSVVGAKYLPGCCNRVLGIPHSSIMGYNFSLLGLEEIIYIVLVLDTVGAGNGMIG 360  
QY 361 FOVLISIGELSLAIVALTSGLLTGLLNKIKRKAPEAKYFDDQVFWKPHLAVGF 417  
DB 361 FOVLISIGELSLAIVALTSGLLTGLLNKIKRKAPEAKYFDDQVFWKPHLAVGF 417

RESULT 8  
Q6A1H3 PRELIMINARY; PRT; 417 AA.  
ID Q6A1H3  
AC Q6A1H3  
DT 25-OCT-2004 (TReMBLrel. 28, Created)  
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
DE Rhesus Blood group D antigen (Fragment).  
GN Name=RHD;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Peripheral blood;  
RA Doeschner A., Wagner F., Schunter F., Petershofen E.K.;  
RT "Four new RHD alleles with previously unknown polymorphism";  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ784310; CAH04920.1; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR InterPro; IPR011058; Cytochrome-N.  
DR InterPro; IPR002229; RhesusRD.  
DR InterPro; IPR010256; RH\_like\_transp.  
DR Pfam; PF00909; Ammonium\_transp; I.  
DR PRINTS; PR00342; RHEUSRD.  
FT NON TER 1  
FT NON TER 1  
SQ SEQUENCE 417 AA; 45146 MW; 649F1358664AF7DB CRC64;

Query Match 92.9%; Score 1974; DB 2; Length 417;  
Best Local Similarity 95.0%; Pred. No. 2.9e-134;  
Matches 396; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSCKYPSVORCLPLCALTEALILFFFTHYDASLEDOKGLVASYQVGODLTWMAI 60  
DB 1 MSCKYPSVORCLPLMALTEALILFFFTHYDASLEDOKGLVASYQVGODLTWMAI 60  
QY 61 GLGFLTSSFRHSHSSVAFNLFMLALGVQWAILLDGFLSOPPSGKVITLFSILATMSA 120  
DB 61 GLGFLTSSFRHSHSSVAFNLFMLALGVQWAILLDGFLSOPPSGKVITLFSILATMSA 120  
QY 121 LSVLISVDVAVGKVNLAQLVVWVLVEVTDLGNLRVINSINFTDYHNMNMHIYFAAYFG 180  
DB 121 LSVLISVDVAVGKVNLAQLVVWVLVEVTDLGNLRVINSINFTDYHNMNMHIYFAAYFG 180  
QY 181 LTVAMCLPKPLPEGTEDNDORATIPSLAMLGALFLMFRPSVNSALLRSPIERKNAVEN 240

```

Db      181 LSVAMCLPKLPBEGEDKQOTATIPSLSMGLFLFMFWPNSNLSLSPERKNAVN 240
Qy      241 TTYAAVAVSVTTAISGSSLAHPQCKISKTYYGSHSAVLEPGVAVDTSCHLIPSPMLPIYGLV 300
Db      241 TTYAAVAVSVTTAISGSSLAHPQCKISKTYYGSHSAVLAGVAVGTSCHLIPSPMLAVLGLV 300
Qy      301 AGLISVGAAYLPGCCNRVLGIPHSSIMGNFSLGLBEIIYIVLVLDVTYGAAGNMIG 360
Db      301 AGLISVGAAYLPGCCNRVLGIPHSSIMGNFSLGLBEIIYIVLVLDVTYGAAGNMIG 360
Qy      361 FOVLSTIGELSLAIVIALTSGLLTALLNLKIRKAPHEAKYFDDQVFWKPHLAVGF 417
Db      361 FOVLSTIGELSLAIVIALTSGLLTALLNLKIRKAPHEAKYFDDQVFWKPHLAVGF 417

```

## RESULT 9

```

O6A1H4 ID O6A1H4 PRELIMINARY; PRT; 417 AA.
AC      25-OCT-2004 (TREMBlrel. 28, Created)
DT      25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT      25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE      Rhesus blood group D antigen (Fragment).
GN      Name=RHD;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxId=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Peripheral blood;
RA      Doescher A., Wagner F., Schunter F., Petershofen E.K.;
RL      Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AJ784309; CAH04919.1; -
DR      GO: GO:0016020; C:membrane; IEA.
DR      InterPro; IPR011058; CyanoVitrin-N.
DR      InterPro; IPR022229; RhesusRHD.
DR      Pfam; PF00909; Ammonium transp.; 1.
DR      PRINTS; PR00342; RHESUSRHD.
FT      NON_TER 1
FT      NON_TER 417
SQ      SEQUENCE 417 AA; 45171 MW; 449F15CA664AF365 CRC64;

```

```

Query Match      92.8%; Score 1972; DB 2; Length 417;
Best Local Similarity 95.0%; Pred. No. 4e-134;
Matches 396; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

```

```

Qy      1 MSCKYPPRSVQRCLPCLATLEALILFLFFTHYDASLEDDKGLVASVYQGDULTVMAAI 60
Db      1 MSCKYPPRSVQRCLPCLATLEALILFLFFTHYDASLEDDKGLVASVYQGDULTVMAAI 60
Qy      61 GLGFLTSSFRHRSWSVAFNLFMLALGVQWAILDDGFLSQPSPGKVITLFSIRLATMSA 120
Db      61 GLGFLTSSFRHRSWSVAFNLFMLALGVQWAILDDGFLSQPSPGKVITLFSIRLATMSA 120
Qy      121 LSVLISVDAVIGKVNLAQLVVMVLVEVTLGNLBMVINSINFTDYHNMNMHIYVFAAYFG 180
Db      121 LSVLISVDAVIGKVNLAQLVVMVLVEVTLGNLBMVINSINFTDYHNMNMHIYVFAAYFG 180
Qy      181 LTVAMCLPKLPBEGEDKQOTATIPSLSAMGLFLFMFWPNSNLSLSPERKNAVN 240
Db      181 LTVAMCLPKLPBEGEDKQOTATIPSLSAMGLFLFMFWPNSNLSLSPERKNAVN 240
Qy      241 TTYAAVAVSVTTAISGSSLAHPQCKISKTYYGSHSAVLEPGVAVDTSCHLIPSPMLPIYGLV 300
Db      241 TTYAAVAVSVTTAISGSSLAHPQCKISKTYYGSHSAVLAGVAVGTSCHLIPSPMLAVLGLV 300
Qy      301 AGLISVGAAYLPGCCNRVLGIPHSSIMGNFSLGLBEIIYIVLVLDVTYGAAGNMIG 360
Db      301 AGLISVGAAYLPGCCNRVLGIPHSSIMGNFSLGLBEIIYIVLVLDVTYGAAGNMIG 360

```

```

Qy      361 FOVLSTIGELSLAIVIALTSGLLTALLNLKIRKAPHEAKYFDDQVFWKPHLAVGF 417
Db      361 FOVLSTIGELSLAIVIALTSGLLTALLNLKIRKAPHEAKYFDDQVFWKPHLAVGF 417

```

## RESULT 10

```

O9NXV8 ID O9NXV8 PRELIMINARY; PRT; 417 AA.
AC      01-OCT-2000 (TREMBlrel. 15, Created)
DT      01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT      01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE      Rhesus blood group D antigen.
GN      Name=RHD;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxId=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Wagner F.F., Flegel W.A.;
RL      Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AJ287289; CAB75731.1; -
DR      EMBL; AJ287290; CAB75731.1; JOINED.
DR      EMBL; AJ287291; CAB75731.1; JOINED.
DR      EMBL; AJ287292; CAB75731.1; JOINED.
DR      EMBL; AJ287293; CAB75731.1; JOINED.
DR      EMBL; AJ287294; CAB75731.1; JOINED.
DR      EMBL; AJ287295; CAB75731.1; JOINED.
DR      EMBL; AJ287296; CAB75731.1; JOINED.
DR      EMBL; AJ287297; CAB75731.1; JOINED.
DR      EMBL; AJ287298; CAB75731.1; JOINED.
DR      GO: GO:0016020; C:membrane; IEA.
DR      InterPro; IPR011058; CyanoVitrin-N.
DR      InterPro; IPR022229; RhesusRHD.
DR      Pfam; PF00909; Ammonium transp.; 1.
DR      PRINTS; PR00342; RHESUSRHD.
SQ      SEQUENCE 417 AA; 45210 MW; 60FB4CFB16F163EF CRC64;

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Query Match      92.8%; Score 1972; DB 2; Length 417;
Best Local Similarity 95.0%; Pred. No. 4e-134;
Matches 396; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

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Qy      1 MSCKYPPRSVQRCLPCLATLEALILFLFFTHYDASLEDDKGLVASVYQGDULTVMAAI 60
Db      1 MSCKYPPRSVQRCLPCLATLEALILFLFFTHYDASLEDDKGLVASVYQGDULTVMAAI 60
Qy      61 GLGFLTSSFRHRSWSVAFNLFMLALGVQWAILDDGFLSQPSPGKVITLFSIRLATMSA 120
Db      61 GLGFLTSSFRHRSWSVAFNLFMLALGVQWAILDDGFLSQPSPGKVITLFSIRLATMSA 120
Qy      121 LSVLISVDAVIGKVNLAQLVVMVLVEVTLGNLBMVINSINFTDYHNMNMHIYVFAAYFG 180
Db      121 LSVLISVDAVIGKVNLAQLVVMVLVEVTLGNLBMVINSINFTDYHNMNMHIYVFAAYFG 180
Qy      181 LTVAMCLPKLPBEGEDKQOTATIPSLSAMGLFLFMFWPNSNLSLSPERKNAVN 240
Db      181 LTVAMCLPKLPBEGEDKQOTATIPSLSAMGLFLFMFWPNSNLSLSPERKNAVN 240
Qy      241 TTYAAVAVSVTTAISGSSLAHPQCKISKTYYGSHSAVLEPGVAVDTSCHLIPSPMLPIYGLV 300
Db      241 TTYAAVAVSVTTAISGSSLAHPQCKISKTYYGSHSAVLAGVAVGTSCHLIPSPMLAVLGLV 300
Qy      301 AGLISVGAAYLPGCCNRVLGIPHSSIMGNFSLGLBEIIYIVLVLDVTYGAAGNMIG 360
Db      301 AGLISVGAAYLPGCCNRVLGIPHSSIMGNFSLGLBEIIYIVLVLDVTYGAAGNMIG 360
Qy      361 FOVLSTIGELSLAIVIALTSGLLTALLNLKIRKAPHEAKYFDDQVFWKPHLAVGF 417
Db      361 FOVLSTIGELSLAIVIALTSGLLTALLNLKIRKAPHEAKYFDDQVFWKPHLAVGF 417

```

```
RESULT 11
06SV88      PRELIMINARY;      PRT;      417 AA.
ID 06SV88;
AC 06SV88;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Rhesus blood group D antigen DRO (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Noizat-Pirenne F., Ansart-Pirenne H.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY449384; AAR24081.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR01058; Cytochrome-N.
DR InterPro; IPR002229; RhesusRD.
DR Pfam; PF00909; Ammonium_transp; 1.
DR PRINTS; PR00342; RHEUSRD.
DR NON TBR
SQ SEQUENCE 417 AA; 45148 MW; C85A4464DBDAF68D CRC64;

Query Match      92.8%; Score 1971; DB 2; Length 417;
Best Local Similarity 94.7%; Pred. No. 4,7e-134;
Matches 395; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSCKYPSVORCLPLCALTLTEALILLFYFPTHYDASLEDOKGLVASVYQVGDLTWAAI 60
DB 1 MSCKYPSVORCLPLCALTLTEALILLFYFPTHYDASLEDOKGLVASVYQVGDLTWAAI 60
QY 61 GLGFLTSSFRHSSVAFLFMLALGVQWAILLDGFLSQPSGKVITLFSITLATMSA 120
DB 61 GLGFLTSSFRHSSVAFLFMLALGVQWAILLDGFLSQPSGKVITLFSITLATMSA 120
QY 121 LSVLISYDAVLGKYNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNHIIYFAAYFG 180
DB 121 LSVLISYDAVLGKYNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNHIIYFAAYFG 180
QY 121 LSVLISYDAVLGKYNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNHIIYFAAYFG 180
DB 121 LSVLISYDAVLGKYNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNHIIYFAAYFG 180
QY 181 LTYAVMCLPKLPBGTEDNDQRTATIPSLAMLGALFLMFPSPVNSALLRSPIRKNAVFN 240
DB 181 LTYAVMCLPKLPBGTEDNDQRTATIPSLAMLGALFLMFPSPVNSALLRSPIRKNAVFN 240
QY 241 TYAAVAVSVTTAISGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIYGLV 300
DB 241 TYAAVAVSVTTAISGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIYGLV 300
QY 241 TYAAVAVSVTTAISGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIYGLV 300
DB 241 TYAAVAVSVTTAISGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIYGLV 300
QY 301 AGLISVGAKYLPGCCNCRVLGIPHSSIMGYNFSLGLLEIITVLLVLDVTGANGMIG 360
DB 301 AGLISVGAKYLPGCCNCRVLGIPHSSIMGYNFSLGLLEIITVLLVLDVTGANGMIG 360
QY 301 AGLISVGAKYLPGCCNCRVLGIPHSSIMGYNFSLGLLEIITVLLVLDVTGANGMIG 360
DB 301 AGLISVGAKYLPGCCNCRVLGIPHSSIMGYNFSLGLLEIITVLLVLDVTGANGMIG 360
QY 361 FOVLISIGELSLAIVIALTSGLLTALLLNKIRAPHEAKYFPDQVFWKPHLAVGF 417
DB 361 FOVLISIGELSLAIVIALTSGLLTALLLNKIRAPHEAKYFPDQVFWKPHLAVGF 417
DB 361 FOVLISIGELSLAIVIALTSGLLTALLLNKIRAPHEAKYFPDQVFWKPHLAVGF 417

RESULT 12
08IZT0      PRELIMINARY;      PRT;      417 AA.
ID 08IZT0;
AC 08IZT0;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Rhesus blood group D antigen D (674) variant.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE=22320945; PubMed=12393640; DOI=10.1182/blood-2002-01-0229;
RA Noizat-Pirenne F., Lee K., Le Penne P.Y., Simon P., Kazup P.,
RA Bachir D., Rouzard A.M., Roussel M., Juszcak G., Menanteau C.,
RA Rouger P., Kotb R., Cartton J.P., Ansart-Pirenne H.;
RT "Rare RHEC phenotypes in black individuals of Afro-Caribbean origin:
RT identification and transfusion safety."
RL Blood 100:4223-4231 (2002).
DR EMBL; AF510070; AAN75126.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR01058; Cytochrome-N.
DR InterPro; IPR002229; RhesusRD.
DR InterPro; IPR010256; RH_like_transp.
DR Pfam; PF00909; Ammonium_transp; 1.
DR PRINTS; PR00342; RHEUSRD.
SQ SEQUENCE 417 AA; 45222 MW; 85241934D7F382D0 CRC64;

Query Match      92.7%; Score 1970; DB 2; Length 417;
Best Local Similarity 94.7%; Pred. No. 5,6e-134;
Matches 395; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSCKYPSVORCLPLCALTLTEALILLFYFPTHYDASLEDOKGLVASVYQVGDLTWAAI 60
DB 1 MSCKYPSVORCLPLCALTLTEALILLFYFPTHYDASLEDOKGLVASVYQVGDLTWAAI 60
QY 61 GLGFLTSSFRHSSVAFLFMLALGVQWAILLDGFLSQPSGKVITLFSITLATMSA 120
DB 61 GLGFLTSSFRHSSVAFLFMLALGVQWAILLDGFLSQPSGKVITLFSITLATMSA 120
QY 121 LSVLISYDAVLGKYNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNHIIYFAAYFG 180
DB 121 LSVLISYDAVLGKYNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNHIIYFAAYFG 180
QY 121 LSVLISYDAVLGKYNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNHIIYFAAYFG 180
DB 121 LSVLISYDAVLGKYNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNHIIYFAAYFG 180
QY 181 LTYAVMCLPKLPBGTEDNDQRTATIPSLAMLGALFLMFPSPVNSALLRSPIRKNAVFN 240
DB 181 LTYAVMCLPKLPBGTEDNDQRTATIPSLAMLGALFLMFPSPVNSALLRSPIRKNAVFN 240
QY 241 TYAAVAVSVTTAISGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIYGLV 300
DB 241 TYAAVAVSVTTAISGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIYGLV 300
QY 241 TYAAVAVSVTTAISGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIYGLV 300
DB 241 TYAAVAVSVTTAISGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIYGLV 300
QY 301 AGLISVGAKYLPGCCNCRVLGIPHSSIMGYNFSLGLLEIITVLLVLDVTGANGMIG 360
DB 301 AGLISVGAKYLPGCCNCRVLGIPHSSIMGYNFSLGLLEIITVLLVLDVTGANGMIG 360
QY 301 AGLISVGAKYLPGCCNCRVLGIPHSSIMGYNFSLGLLEIITVLLVLDVTGANGMIG 360
DB 301 AGLISVGAKYLPGCCNCRVLGIPHSSIMGYNFSLGLLEIITVLLVLDVTGANGMIG 360
QY 361 FOVLISIGELSLAIVIALTSGLLTALLLNKIRAPHEAKYFPDQVFWKPHLAVGF 417
DB 361 FOVLISIGELSLAIVIALTSGLLTALLLNKIRAPHEAKYFPDQVFWKPHLAVGF 417
DB 361 FOVLISIGELSLAIVIALTSGLLTALLLNKIRAPHEAKYFPDQVFWKPHLAVGF 417

RESULT 13
06SV90      PRELIMINARY;      PRT;      417 AA.
ID 06SV90;
AC 06SV90;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Rhesus blood group D antigen DLO (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Noizat-Pirenne F., Ansart-Pirenne H.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY449382; AAR24079.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR01058; Cytochrome-N.
DR InterPro; IPR002229; RhesusRD.
DR Pfam; PF00909; Ammonium_transp; 1.
DR PRINTS; PR00342; RHEUSRD.
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FT  NON TER      417      417
SQ  SEQUENCE     417 AA;  45188 MW;  0B49654D7994CIDE CRC64;

Query Match
Best Local Similarity  92.7%; Score 1970; DB 2; Length 417;
Matches 395; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

QY  1 MSCKYPRSVQRCPLFCATLTLEAAILLFFFTHYDASLEDOKGLVASVQVODLTVMMAI 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  1 MSCKYPRSVQRCPLFCATLTLEAAILLFFFTHYDASLEDOKGLVASVQVODLTVMMAI 60
QY  61 GIGFLTSSFRHSWSSVAFNLFMALGVQWAILLDGFLSQPSPGKVITLFSIWLATMSA 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  61 GIGFLTSSFRHSWSSVAFNLFMALGVQWAILLDGFLSQPSPGKVITLFSIWLATMSA 120
QY  121 LSVLISVDVAVLGVKNIQAQLVVMVLVEVTDLGNLRMVINSINFTDYHNMNMHIYVFAAYFG 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  121 LSVLISVDVAVLGVKNIQAQLVVMVLVEVTDLGNLRMVINSINFTDYHNMNMHIYVFAAYFG 180
QY  181 LTVAMCLPKPLPEGTEDNDQATIPSLSNMGLFLMFRPSVNSALLRSPIERKNAVEN 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  181 LTVAMCLPKPLPEGTEDNDQATIPSLSNMGLFLMFRPSVNSALLRSPIERKNAVEN 240
QY  241 TYVAAVSVVTAISGSSLAHPQGIKSTYVHSVAVLGGVAVGTLCILIPSPWLAMVLGLV 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  241 TYVAAVSVVTAISGSSLAHPQGIKSTYVHSVAVLGGVAVGTLCILIPSPWLAMVLGLV 300
QY  301 AGLISVRGAKYLPGCCNRVLGIPHSIMGVNFSLLGLEIIYIVLLVLDTVGAGNGMTG 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  301 AGLISVRGAKYLPGCCNRVLGIPHSIMGVNFSLLGLEIIYIVLLVLDTVGAGNGMTG 360
QY  361 FOVLISIGELSLAIVIALTSGLLTALLNLKIRKAPHEAKYFDDQVFMKPHLAVGF 417
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  361 FOVLISIGELSLAIVIALTSGLLTALLNLKIRKAPHEAKYFDDQVFMKPHLAVGF 417

RESULT 14
Q6SV87 PRELIMINARY; PRT; 417 AA.
AC Q6SV87;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Rhesus blood group D antigen DBA (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Noizat-Pirenne F.; Ansart-Pirenne H.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY449385; AAR24082.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR011058; Cyanovirin-N.
DR InterPro; IPR003229; RhesusRHD.
DR InterPro; IPR010256; RH_like_transpt.
DR Pfam; PF00909; Ammonium_transp; 1.
DR PRINTS; PR00342; RHESUSRHD.
FT NON TER      417
SQ SEQUENCE     417 AA;  45146 MW;  C37E02699A8BE890 CRC64;

Query Match
Best Local Similarity  92.7%; Score 1969; DB 2; Length 417;
Matches 395; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

QY  1 MSCKYPRSVQRCPLFCATLTLEAAILLFFFTHYDASLEDOKGLVASVQVODLTVMMAI 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  1 MSCKYPRSVQRCPLFCATLTLEAAILLFFFTHYDASLEDOKGLVASVQVODLTVMMAI 60
QY  61 GIGFLTSSFRHSWSSVAFNLFMALGVQWAILLDGFLSQPSPGKVITLFSIWLATMSA 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  61 GIGFLTSSFRHSWSSVAFNLFMALGVQWAILLDGFLSQPSPGKVITLFSIWLATMSA 120
QY  121 LSVLISVDVAVLGVKNIQAQLVVMVLVEVTDLGNLRMVINSINFTDYHNMNMHIYVFAAYFG 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  121 LSVLISVDVAVLGVKNIQAQLVVMVLVEVTDLGNLRMVINSINFTDYHNMNMHIYVFAAYFG 180
QY  181 LTVAMCLPKPLPEGTEDNDQATIPSLSNMGLFLMFRPSVNSALLRSPIERKNAVEN 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  181 LTVAMCLPKPLPEGTEDNDQATIPSLSNMGLFLMFRPSVNSALLRSPIERKNAVEN 240
QY  241 TYVAAVSVVTAISGSSLAHPQGIKSTYVHSVAVLGGVAVGTLCILIPSPWLAMVLGLV 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  241 TYVAAVSVVTAISGSSLAHPQGIKSTYVHSVAVLGGVAVGTLCILIPSPWLAMVLGLV 300
QY  301 AGLISVRGAKYLPGCCNRVLGIPHSIMGVNFSLLGLEIIYIVLLVLDTVGAGNGMTG 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  301 AGLISVRGAKYLPGCCNRVLGIPHSIMGVNFSLLGLEIIYIVLLVLDTVGAGNGMTG 360
QY  361 FOVLISIGELSLAIVIALTSGLLTALLNLKIRKAPHEAKYFDDQVFMKPHLAVGF 417
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  361 FOVLISIGELSLAIVIALTSGLLTALLNLKIRKAPHEAKYFDDQVFMKPHLAVGF 417

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QY  121 LSVLISVDVAVLGVKNIQAQLVVMVLVEVTDLGNLRMVINSINFTDYHNMNMHIYVFAAYFG 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  121 LSVLISVDVAVLGVKNIQAQLVVMVLVEVTDLGNLRMVINSINFTDYHNMNMHIYVFAAYFG 180
QY  181 LTVAMCLPKPLPEGTEDNDQATIPSLSNMGLFLMFRPSVNSALLRSPIERKNAVEN 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  181 LTVAMCLPKPLPEGTEDNDQATIPSLSNMGLFLMFRPSVNSALLRSPIERKNAVEN 240
QY  241 TYVAAVSVVTAISGSSLAHPQGIKSTYVHSVAVLGGVAVGTLCILIPSPWLAMVLGLV 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  241 TYVAAVSVVTAISGSSLAHPQGIKSTYVHSVAVLGGVAVGTLCILIPSPWLAMVLGLV 300
QY  301 AGLISVRGAKYLPGCCNRVLGIPHSIMGVNFSLLGLEIIYIVLLVLDTVGAGNGMTG 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  301 AGLISVRGAKYLPGCCNRVLGIPHSIMGVNFSLLGLEIIYIVLLVLDTVGAGNGMTG 360
QY  361 FOVLISIGELSLAIVIALTSGLLTALLNLKIRKAPHEAKYFDDQVFMKPHLAVGF 417
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  361 FOVLISIGELSLAIVIALTSGLLTALLNLKIRKAPHEAKYFDDQVFMKPHLAVGF 417

RESULT 15
Q6SV91 PRELIMINARY; PRT; 417 AA.
AC Q6SV91;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Rhesus blood group D antigen DBA (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Noizat-Pirenne F.; Ansart-Pirenne H.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY449381; AAR24078.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR011058; Cyanovirin-N.
DR InterPro; IPR002229; RhesusRHD.
DR InterPro; IPR010256; RH_like_transpt.
DR Pfam; PF00909; Ammonium_transp; 1.
DR PRINTS; PR00342; RHESUSRHD.
FT NON TER      417
SQ SEQUENCE     417 AA;  45220 MW;  C84B08C4780D3DCC CRC64;

Query Match
Best Local Similarity  92.7%; Score 1969; DB 2; Length 417;
Matches 395; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

QY  1 MSCKYPRSVQRCPLFCATLTLEAAILLFFFTHYDASLEDOKGLVASVQVODLTVMMAI 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  1 MSCKYPRSVQRCPLFCATLTLEAAILLFFFTHYDASLEDOKGLVASVQVODLTVMMAI 60
QY  61 GIGFLTSSFRHSWSSVAFNLFMALGVQWAILLDGFLSQPSPGKVITLFSIWLATMSA 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  61 GIGFLTSSFRHSWSSVAFNLFMALGVQWAILLDGFLSQPSPGKVITLFSIWLATMSA 120
QY  121 LSVLISVDVAVLGVKNIQAQLVVMVLVEVTDLGNLRMVINSINFTDYHNMNMHIYVFAAYFG 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  121 LSVLISVDVAVLGVKNIQAQLVVMVLVEVTDLGNLRMVINSINFTDYHNMNMHIYVFAAYFG 180
QY  181 LTVAMCLPKPLPEGTEDNDQATIPSLSNMGLFLMFRPSVNSALLRSPIERKNAVEN 240
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  181 LTVAMCLPKPLPEGTEDNDQATIPSLSNMGLFLMFRPSVNSALLRSPIERKNAVEN 240
QY  241 TYVAAVSVVTAISGSSLAHPQGIKSTYVHSVAVLGGVAVGTLCILIPSPWLAMVLGLV 300
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  241 TYVAAVSVVTAISGSSLAHPQGIKSTYVHSVAVLGGVAVGTLCILIPSPWLAMVLGLV 300
QY  301 AGLISVRGAKYLPGCCNRVLGIPHSIMGVNFSLLGLEIIYIVLLVLDTVGAGNGMTG 360
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  301 AGLISVRGAKYLPGCCNRVLGIPHSIMGVNFSLLGLEIIYIVLLVLDTVGAGNGMTG 360
QY  361 FOVLISIGELSLAIVIALTSGLLTALLNLKIRKAPHEAKYFDDQVFMKPHLAVGF 417
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  361 FOVLISIGELSLAIVIALTSGLLTALLNLKIRKAPHEAKYFDDQVFMKPHLAVGF 417

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Db	301	AGLISVGAKYLRPCCNRVLGIPHSIMGYNFSLSGLGRIYIVLVLDIVGANGMIG	360
QY	361	FQVLLSIGELSLAIVIALTSGLLTALLLNKIRKAPHEAKYFDDQVFWKPPHLAVGF	417
Db	361	FQVLLSIGELSLAIVIALTSGLLTALLLNKIRKAPHEAKYFDDQVFWKPPHLAVGF	417

Search completed: March 24, 2005, 13:18:18  
Job time : 70 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 24, 2005, 13:13:45 ; Search time 164 Seconds  
(without alignments)  
983.409 Million cell updates/sec

Title: CAC07879  
Perfect score: 2124  
Sequence: 1 MSCKPRSVGRCLPLCALTL.....EAKYFDQVFWKPHLVAGF 417

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980a:\*  
2: geneseqp1990a:\*  
3: geneseqp2000a:\*  
4: geneseqp2001a:\*  
5: geneseqp2002a:\*  
6: geneseqp2003a:\*  
7: geneseqp2003ba:\*  
8: geneseqp2004a:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
1	1982	93.3	417	3	AAB03341	Aab03341 Human Rhd
2	1980	93.2	417	2	AAV24056	Aav24056 Protein e
3	1975	93.0	416	7	ADBS4449	Adbs4449 Human Pro
4	1975	93.0	416	7	ADDA5097	Adda5097 Human Pro
5	1975	93.0	416	7	ADBS4445	Adbs4445 Human Pro
6	1932	91.0	417	7	ADDA6525	Adda6525 Human Pro
7	1932	91.0	417	7	ADDA6529	Adda6529 Human Pro
8	1859	87.5	417	3	AA803339	Aa803339 Human Rhc
9	1854	87.3	417	3	AA803338	Aa803338 Human Rhc
10	1838	86.5	417	3	AA803342	Aa803342 Human Rhc
11	1833	86.3	417	3	AA803340	Aa803340 Human Rhc
12	1605	75.6	401	8	ADR09337	Adr09337 Human pro
13	991.5	46.7	422	7	ADDA6523	Adda6523 Rat Prote
14	991.5	46.7	422	7	ADBS4447	Adbs4447 Rat Prote
15	991.5	46.7	422	7	ADBS4444	Adbs4444 Rat Prote
16	991.5	46.7	422	7	ADDA5095	Adda5095 Rat Prote
17	991.5	46.7	422	7	ADDA6527	Adda6527 Rat Prote
18	913.5	43.0	209	8	ADP29742	Adp29742 Human sec
19	882	41.5	214	8	ADP29742	Adp29742 Human sec
20	497	23.4	473	3	AA842135	Aa842135 Human ORF
21	497	23.4	479	4	AA829656	Aa829656 Human mem
22	497	23.4	479	4	AA837000	Aa837000 Oesophagu
23	497	23.4	479	5	AAU78997	Aau78997 Human Rh
24	497	23.4	479	6	ABU56530	Abu56530 Lung canc
25	497	23.4	479	8	ADN04910	Adn04910 Antipori

26	490	23.1	445	6	AB015004	Ab015004 Human NOV
27	488.5	23.0	498	5	AAU78998	Aau78998 Mouse Rh
28	480.5	22.6	455	5	AAU78092	Aau78092 Mouse non
29	476	22.4	324	7	ADJ69283	Adj69283 Human hea
30	466.5	22.0	458	5	AAU78091	Aau78091 Human non
31	418.5	19.7	441	5	ABP69263	Abp69263 Human pol
32	417	19.6	449	4	ABBS7883	Abbs7883 Drosoph11
33	374	17.6	448	5	AAE18217	Aae18217 Human MOL
34	374	17.6	448	7	ADJ18217	Adj18217 Human mol
35	362.5	17.1	395	7	ADJ08355	Adj08355 Novel pro
36	302	14.2	326	5	ABBS9036	Abbs9036 Human pol
37	257	12.1	54	4	AAAM15110	Aam15110 Peptide #
38	257	12.1	54	4	ABBS4104	Abbs4104 Peptide #
39	257	12.1	54	4	AAW27565	Aaw27565 Peptide #
40	257	12.1	54	4	ABR28933	Abbr28933 Peptide #
41	257	12.1	54	4	ABBI9542	Abbi9542 Protein #
42	257	12.1	54	4	AAW67271	Aaw67271 Human bon
43	257	12.1	54	4	AAW54889	Aaw54889 Human bra
44	257	12.1	54	4	ABG48932	Abg48932 Human liv
45	257	12.1	54	4	AAW02851	Aaw02851 Peptide #

## ALIGNMENTS

RESULT 1  
AAB03341  
ID AAB03341 standard; protein; 417 AA.  
AC AAB03341;  
XX  
DT 26-SEP-2000 (first entry)  
XX  
DE Human Rhd protein.  
XX  
XX Human; rhesus blood group system; Rh; Rhd; RHCE; sickle cell disease;  
KW thalassemia; Rhc; Rnc; RHe; Rhe; alloimmunisation prevention;  
KW autoimmune Rh haemolytic disease; rhesus protein; immunosuppressive;  
KW vaccine.  
XX  
OS Homo sapiens.  
XX  
PN WO200032632-A2.  
XX  
PD 08-JUN-2000.  
XX  
PF 01-DEC-1999; 99WO-GB004027.  
XX  
PR 01-DEC-1998; 98GB-00026378.  
XX  
PA (UYAB-) UNTV ABERDEEN.  
XX  
PA (COMM-) COMMON SERVICES AGENCY SCOTTISH HEALTH S.  
XX  
PI Urbanlak SJ, Barker RN;  
XX  
DR MPI; 2000-412291/35.  
XX  
PT Composition for prevention of alloimmunization or immunosuppression of a  
XX response elicited by alloimmunization or an autoimmune hemolytic disease,  
XX comprises an epitope of a rhesus protein.  
XX  
PS Disclosure; Page 88-90; 92pp; English.  
XX  
XX Human blood contains the rhesus (Rh) blood group system, and humans can  
XX either be RhD positive or negative. This can lead to complications during  
XX transfusions or pregnancy if RhD negative individuals are exposed to RhD  
XX positive blood, leading to them becoming immunised to produce anti-D. The  
XX present invention relates to new human allo- and auto-reactive T-cell  
XX epitopes (AAV99760-Y99769 and AAB03201-B03337) from Rhd, Rhc, Rnc, RHe  
XX and Rne proteins. These epitopes bind to T-cells to elicit an immune  
XX response, i.e. immunisation. These epitopes can be used as a vaccine for  
XX the prevention of alloimmunisation or immunosuppression of a response  
XX elicited by alloimmunisation or an autoimmune haemolytic disease.

CC Examples of autoimmune haemolytic diseases are sickle cell disease and  
CC thalassemia. The present sequence is the human Rhd protein from which  
CC the epitopes in the present invention were derived  
XX

SO Sequence 417 AA;

Query Match 93.3%; Score 1982; DB 3; Length 417;  
Best Local Similarity 95.2%; Pred. No. 4.4e-184;  
Matches 397; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 MSCKYRSVORCLPLCALTLLEAALLILFFFFHYDASLEDQGLVASYQVGODLTVMMAI 60  
DB 1 MSCKYRSVORCLPLCALTLLEAALLILFFFFHYDASLEDQGLVASYQVGODLTVMMAI 60  
QY 61 GLGFLTSPFRHSSWSSVAFNLFMLAGVOMATILDGFLSOPSGKVITLPSIMLATMSA 120  
DB 61 GLGFLTSPFRHSSWSSVAFNLFMLAGVOMATILDGFLSOPSGKVITLPSIRLATMSA 120  
QY 121 LSVLISVDVAVLGKVNLAQLVWVAVLVETDLGNLRVVISNIFNTDYHMMMHIIYFAAYFG 180  
DB 121 LSVLISVDVAVLGKVNLAQLVWVAVLVETDLGNLRVVISNIFNTDYHMMMHIIYFAAYFG 180  
QY 181 LTVAMCLPKPLPEGTEDNDORATIPSLSAMLGALFLMFRPSVNSALLRSPIERKNVFN 240  
DB 181 LTVAMCLPKPLPEGTEDNDORATIPSLSAMLGALFLMFRPSVNSALLRSPIERKNVFN 240  
QY 241 TYAAVAVSVVTAISGSSLAHPQGIKSTYGHSAVLPBGAAVDTSCHLIPSPMLPIVLGLV 300  
DB 241 TYAAVAVSVVTAISGSSLAHPQGIKSTYGHSAVLPBGAAVDTSCHLIPSPMLPIVLGLV 300  
QY 301 AGLISVRAKYLPGCCNVLGIPIHSSINGNPSLGLLEIITLYVLVLDTVGAGNGMIG 360  
DB 301 AGLISVRAKYLPGCCNVLGIPIHSSINGNPSLGLLEIITLYVLVLDTVGAGNGMIG 360  
QY 361 FOVLISIGELSLAIVALTSGLTGLNLNLKIRKAPHEAKYFDQVFWKPFHLAVGF 417  
DB 361 FOVLISIGELSLAIVALTSGLTGLNLNLKIRKAPHEAKYFDQVFWKPFHLAVGF 417

RESULT 2

AAV24056 standard; protein; 417 AA.

AAV24056;

04-OCT-1999 (first entry)

Protein encoded by the prevalent allele of the Rhd gene.

Allele; Rhesus D antigen; Rhd; weak D phenotype; blood transfusion.

Homo sapiens.

MO9937763-A2.

29-JUL-1999.

18-DEC-1998; 98MO-EP008319.

23-JAN-1998; 98EP-00101203.

(DRKB-) DRK BLUTSPENDEIENST BADEN WUERTTEMBERG.

Flegel WA, Wagner FF;

WPI; 1999-469127/39.

N-PSDB; AAX86522.

Nucleic acid sequences correlated with Rhesus weak D phenotype, useful  
PT for screening blood from donors and recipients for transfusion methods.

Disclosure; Fig 2; 64pp; English.

CC The present sequence is encoded by the prevalent allele of the Rhesus D  
CC (Rhd) antigen gene. The specification describes a Rhd contributing to or  
CC indicative of the weak D phenotype, where the Rhd polynucleotide carries  
CC at least one missense mutation as compared to the wild-type Rhd, in its  
CC transmembrane and/or intracellular regions, especially in amino acid  
CC positions 2-16, 114-149, 179-225 or/and 267-397, with the proviso that  
CC the D antigen does not carry a single missense mutation leading to a  
CC F223V or T283I substitution. The probes and antibodies are useful in the  
CC methods for detection of weak D phenotypes. Red blood cells, from  
CC reactants, are useful for the assessment of the affinity, avidity and/or  
CC of anti-globulin or anti-human-globulin antisera. Detecting the presence  
CC of the Rhd associated with weak D phenotype is useful for determining  
CC that a patient in need of a blood transfusion is to be transfused with  
CC Rhd negative blood from a donor. Alternatively, testing for weak D  
CC phenotype Rhd in the blood of a donor is useful for determining whether  
CC the donor blood should be excluded for transfusion to patients having  
CC wild type Rhd or weak D types, other than that of the donor weak D type  
XX

SO Sequence 417 AA;

Query Match 93.2%; Score 1980; DB 2; Length 417;  
Best Local Similarity 95.2%; Pred. No. 6.8e-184;  
Matches 397; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

QY 1 MSCKYRSVORCLPLCALTLLEAALLILFFFFHYDASLEDQGLVASYQVGODLTVMMAI 60  
DB 1 MSCKYRSVORCLPLCALTLLEAALLILFFFFHYDASLEDQGLVASYQVGODLTVMMAI 60  
QY 61 GLGFLTSPFRHSSWSSVAFNLFMLAGVOMATILDGFLSOPSGKVITLPSIMLATMSA 120  
DB 61 GLGFLTSPFRHSSWSSVAFNLFMLAGVOMATILDGFLSOPSGKVITLPSIRLATMSA 120  
QY 121 LSVLISVDVAVLGKVNLAQLVWVAVLVETDLGNLRVVISNIFNTDYHMMMHIIYFAAYFG 180  
DB 121 LSVLISVDVAVLGKVNLAQLVWVAVLVETDLGNLRVVISNIFNTDYHMMMHIIYFAAYFG 180  
QY 181 LTVAMCLPKPLPEGTEDNDORATIPSLSAMLGALFLMFRPSVNSALLRSPIERKNVFN 240  
DB 181 LTVAMCLPKPLPEGTEDNDORATIPSLSAMLGALFLMFRPSVNSALLRSPIERKNVFN 240  
QY 241 TYAAVAVSVVTAISGSSLAHPQGIKSTYGHSAVLPBGAAVDTSCHLIPSPMLPIVLGLV 300  
DB 241 TYAAVAVSVVTAISGSSLAHPQGIKSTYGHSAVLPBGAAVDTSCHLIPSPMLPIVLGLV 300  
QY 301 AGLISVRAKYLPGCCNVLGIPIHSSINGNPSLGLLEIITLYVLVLDTVGAGNGMIG 360  
DB 301 AGLISVRAKYLPGCCNVLGIPIHSSINGNPSLGLLEIITLYVLVLDTVGAGNGMIG 360  
QY 361 FOVLISIGELSLAIVALTSGLTGLNLNLKIRKAPHEAKYFDQVFWKPFHLAVGF 417  
DB 361 FOVLISIGELSLAIVALTSGLTGLNLNLKIRKAPHEAKYFDQVFWKPFHLAVGF 417

RESULT 3

ADE54449 standard; protein; 416 AA.

ADE54449;

29-JAN-2004 (first entry)

Human Protein Q9U021, SEQ ID NO 252.

Human; pain; neuronal tissue; gene therapy;

spinal segmental nerve injury; chronic constriction injury; CCI;

spared nerve injury; SNI; Chung.

Homo sapiens.

MO2003016475-A2.

27-FEB-2003.





ftp.wipo.int/published\_pct\_sequences

Sequence 416 AA;

Query Match

93.0%: Score 1975: DB 7: Length 416.

Best Local Similarity 95.2%; Pred. No. 2.1e-183;  
Matches 196; Conservation 3; Mismatches 17

Matches 396; Conservative 3; Mismatches 17; Indels 0; Gaps 0.

QY	2	SCXKPRSTQORCLPCLALITLLEALILLFFPFTHYDASLEDOQLVASVOYQODLTJMAAIG	61
Db	1	SSKXPRSTQORCLPCLMALITLLEALILLFFPFTHYDASLEDOQLVASVOYQODLTJMAAIG	60
QY	62	LGFLTSSRRRSMSSVAENLFMLAGVOMAILDDOFLSOPSGKAVITLFSJLWTAMAL	121
Db	61	LGFLTSSRRRSMSSVAENLFMLAGVOMAILDDOFLSOPSGKAVITLFSJLWTAMAL	120
QY	122	SVLISVDADVLRKVNLAQULVMVLYEVTDLGNLRVVISNIENFDYHMMNMHIVFAAYEGL	181
Db	121	SVLISVDADVLRKVNLAQULVMVLYEVTALGNLRVVISNIENFDYHMMNMHIVFAAYEGL	180
QY	182	TVAMCCLPKPLEEGEDNDQRTATIBSLSMCLALPLMMPRPVSNAJLPSPIERKCAVNT	241
Db	181	SVAMCCLPKPLEEGEDNDQRTATIBSLSMCLALPLMMPRPVSNAJLPSPIERKCAVNT	240
QY	242	YYAAVAVSVTALISGSSSLAHPOGKISKTYGHSADVLEGAVAVNTSCHLISPMPLPYLGVA	301
Db	241	YYAAVAVSVTALISGSSSLAHPOGKISKTYGHSADVLAGVAVNTSCHLISPMPLAMVLGVA	300
QY	302	GLISVGRKATLPGCCNRVLGIPHSSIMGYNFSLGLEETIYVLLVLDVTGAGNGMIGF	361
Db	301	GLISVGRKATLPGCCNRVLGIPHSSIMGYNFSLGLEETIYVLLVLDVTGAGNGMIGF	360
QY	362	QVLLSIEBELSLATIALTSGLLTALLNLKIRKAPHEKRYDDDOVFMKFPHLANGF	417
Db	361	QVLLSIEBELSLATIALTSGLLTALLNLKIRKAPHEKRYDDDOVFMKFPHLANGF	416

RESULT 5  
ADE54445

ID	ADE54445	standard; protein; 416 AA.
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AC ADE54445;

DT 29-JAN-2004 (first entry)

Human Protein Q9UQ21, SEQ ID NO 248.

**KW** Human; pain; neuronal tissue; gene therapy;

spared nerve injury; SNI; Chung, KW

**Homo sapiens.**

XX WO2003016475-  
PN

XX 27-FEB-2003  
PD

2 XX  
2  
2  
2  
2  
2  
2  
2

XX XX

PR 01-NOV-2001; 2001US-0346382P.

20-NOV-2001; 200105-0333334/P.

PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG

	XX	Woolf C	Dixson D	Baker
	PT			

WDT: 2003 060310/00

XX  
X

PT preparing a medicament

PS Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated nucleic acid sequences, a polynucleotide or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (thung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPD at [ftp.wipo.int/publ/published\\_pct\\_sequences](http://wipo.int/publ/published_pct_sequences).

**SQ** Sequence 416 AA;

Query Match	93.08;	Score 1975;	DB 7;	Length 416;
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Best local similarity 55.26; Fied. NO. 2.1E-183;  
Matches 396; Conservative 3; Mismatches 17;

2 SCKYPRSVORCLPLCALTIEAALITLFYFETHYDASI.EDOKGI.VASVOVGODI.TVMAATG 61

QY	2	SCKYRQVQRCLPTCALTLFEAAILILFFYPFHYSASLEDQGHVASVYQGDLTWAAIG	61
Db	1	SSKYPKSVARCRPLMAALTLEAAILILFFYPFHYSASLEDQGHVASVYQGDLTWAAIG	60
QY	62	LGFLTSSFRHRSSVAFNLFMLALGYQMAILLDGLSOPSPGKVITFTSLWATMSAL	121
Db	61	LGFLTSSFRHRSSVAFNLFMLALGYQMAILLDGLSOPSPGKVITFTSLWATMSAL	120
QY	122	SVLISVDNALGKVNLAQVWVWLVEVETD.LGNLRKRVISINIENTDYHNMWHIYFEAPFGL	181
Db	121	SVLISVDNALGKVNLAQVWVWLVEVETALGNLRKRVISINIENTDYHNMWHIYFEAPFGL	180
QY	182	TYAACLPRPLBEGTIEDNDQRTPTSPISAMIGALFLMWRPDSVNSALLRSPFIERKNAVNT	241
Db	181	SVAMCCKPRPLBEGTIEDKQQTATIPISLAMIAGALFLMWFMPSPFSALLRSPFIERKNAVNT	240
QY	242	YAAVAVSVVVTALISGSSLAHPQGKISKTYGHSAYLPBGVAVDTSCHLIPSPMLPIYVGLVA	301
Db	241	YAAVAVSVVTALISGSSLAHPQGKISKTYHSAYVLAAGVAAGTISCHLIPSPMLAMVGLVA	300
QY	302	GLISVYRGAKYLPGCCNRYLGIPIHSSINGYNFSLGLGLEEIIYIVLVLDTVGAGNGMTGF	361
Db	301	GLISVYRGAKYLPGCCNRYLGIPIHSSINGYNFSLGLGLEEIIYIVLVLDTVGAGNGMTGF	360
QY	362	QVLLSLISGLSLAIYIALTSGLLTLLNLKIRKAPHEAKYFPDQVWPKRPHLAVGF	417
Db	361	QVLLSLISGLSLAIYIALTSGLLTLLNLKIMRAPHEAKYFPDQVWPKRPHLAVGF	416

RESULT 6

ID ADP46525

ADP46525 standard; protein; 417 AA.

AC ADP46525;

XX

XX 02-DEC-2004 (revised)

DT 29-JAN-2004 (first entry)

DT

## RESULT 6

ID ADD46525 standard; protein; 417 AA

AC ADD46525

02-DEC-2004 (revised)

DT 29-JAN-2004 (first entry)

Human Protein CAB09722, SEQ ID NO 12206.

Human; pain; neuronal tissue; gene therapy;  
spinal segmental nerve injury; chronic constriction injury; CCI;  
spared nerve injury; SNI; Chung.

Homo sapiens.  
Unidentified.

WO2003016475-A2.

27-FEB-2003.

14-AUG-2002; 2002WO-US025765.

14-AUG-2001; 2001US-0312147P.  
01-NOV-2001; 2001US-0346382P.  
26-NOV-2001; 2001US-0333347P.

(GEHO ) GEN HOSPITAL CORP.  
(FARB ) BAYER AG.

Woolf C, D'urso D, Befort K, Costigan M;  
WPI; 2003-268312/26.  
GENBANK; CAB09722.

New composition comprising two or more isolated polypeptides, useful for  
preparing a medicament for treating pain in an animal.

Example 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (described in Table 3 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at [http://wipo.int/pub/publ/published\\_pct\\_sequences](http://wipo.int/pub/publ/published_pct_sequences).

Query Match	91.0%	Score 1933;	DB 7;	Length 417;
Best Local Similarity	92.6%	Pred. No. 3.2e-179;		
Matches 386; Conservative	9;	Mismatches 22;	Indels 0;	Gaps 0;

QY I MSCCKPRSYQRCLEPCALTLLEAALLLPFTFYHDASLEDOCKLVASYQGDULTWMAAI 60  
Db 1 MSSKYPKRSVRRCLEPCALTLLEAALLLPFTFYHDASLEDOCKLVASYQGDULTWMAAI 60  
QY 61 GIGPLTSSRRRRSSWVAFLMALAGVOMAILLDGFLSGFPGKAVITTFSTILATMSA 120

Db 61 GLGLFSSFRHSHMSVAFNLFMLAGVQWAILLDGFLSPSPSKAVITLFSIRLATWSA 120

Qy 121 LSVLISVANVYGVKNVLAQVVMVVLVEYDLCGLNRVYISNIFPTMDYMMNMHLYVFAAAYG 180

Db 121 MSVVISAGAVGVKNVLAQVVMVVLVEYVALGTLNRVYISNIFPTMDYMMNRHFVFAAYFG 180

Qy 181 LTVAMCLPEKPLPEGTEDNDORATIPSLSAMGALFLMMRPSVNSALRSPIERKNAVFN 240

Db 181 LTVAMCLPEKPLPEGTEDNDORATIPSLSAMGALFLMMRPSVNSALRSPIERKNAVFN 240

Qy 241 TTYAVANSVVTALISGSSLAHPQKISKITYGSHAVUPEGYAVDTSCHLIESPMPIYVLGY 3000

Db 241 TTYALAVSVVTALISGSSLAHPQKISKITYGSHAVVLAGVAVTSCHLIESPMVLAIVLGLV 3000

Qy 301 AGLISVRGAKYLPGCCNRYLGIPIHSSINGYNFSLGLLEELIYIYVLVLDPTVAGAGMGIG 360

Db 301 AGLISIGAKCLPGCCNRYLGIPIHSSINGYNFSLGLLEELIYIYVLVLDPTVAGAGMGIG 360

Qy 361 FQVLTISIEELSLAYIALTSGLLTLLNLTKRKAPHEAKYRDDDYFWKFRPHLAVGF 417

Db 361 FQVLTISIEELSLAYIALTSGLLTLLNLTKRWKAPHEAKYRDDDYFWKFRPHLAVGF 417

RESULT 7	
ADD46529	
ID	ADD46529 standard; protein; 417 AA
XX	
XX	
AC	ADD46529;
XX	
DT	02-DEC-2004 (revised)
DT	29-JAN-2004 (first entry)

Human Protein CAB09722, SEQ ID NO 12210.

KM Human; pain; neuronal tissue; gene therapy;  
KM spinal segmental nerve injury; chronic constriction injury; CCI;  
KM spared nerve injury; SNI; Chung.

Homo sapiens.  
Unidentified.

PN	WO2003016475-A2.
XX	
PD	27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GEHO ) GEN HOSPITAL CORP

(FARB) BAYER AG.

Woolf C, D'urso D, Befort K, Costigan M;

WPI; 2003-268312/26.

GENBANK; CAB09722.

New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Example 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal

CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (SN1) in an animal (e.g. gene  
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (described in Table 3  
CC of the specification) which is differentially expressed during pain.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

SO Sequence 417 AA;

Query Match 91.0%; Score 1932; DB 7; Length 417;  
Best Local Similarity 92.6%; Pred. No. 3.2e-179; Indels 0; Gaps 0;  
Matches 386; Conservative 9; Mismatches 22;

QY 1 MSCKPRSRVORCLPLCALTLLEAAILLFFFTHYDASLEDQGLVASVYQVQDILTVMMAI 60  
DB 1 MSCKPRSRVORCLPLCALTLLEAAILLFFFTHYDASLEDQGLVASVYQVQDILTVMMAI 60  
QY 61 GIGFTTSFRRHSMSVAFNFMALGVOMAILLDGFLSOPPSGKVITLPSILATMSA 120  
DB 61 GIGFTTSFRRHSMSVAFNFMALGVOMAILLDGFLSOPPSGKVITLPSILATMSA 120  
QY 121 LSVLISVDAVIGKVNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNNMMHIYVFAAYFG 180  
DB 121 MSVLISAGAVIGKVNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNNLRHFFVFAAYFG 180  
QY 181 LTVAMCLPKPLPEGEENDDORATIPSLSAMGALFLMFRPSVNSALLRSPIERKNAVEN 240  
DB 181 LTVAMCLPKPLPEGEENDDORATIPSLSAMGALFLMFRPSVNSALLRSPIERKNAVEN 240  
QY 241 TYVAVAVSVTVAISGSSLAHPQKISMTYVHSATVLAGVAVGTSCHILPSPWLAUUGLV 300  
DB 241 TYVAVAVSVTVAISGSSLAHPQKISMTYVHSATVLAGVAVGTSCHILPSPWLAUUGLV 300  
QY 301 AGLSVRAKYLPGCCNRVIGIPHSSTINGVNFSLGLLEBITYIVLLVDTVGANGMIG 360  
DB 301 AGLSVRAKYLPGCCNRVIGIPHSSTINGVNFSLGLLEBITYIVLLVDTVGANGMIG 360  
QY 361 FOVLISIGELSLAIVIALTSGLTGLLNLKIRKAPHEAKYFPDOVFWRKPHLAVGF 417  
DB 361 FOVLISIGELSLAIVIALTSGLTGLLNLKIRKAPHEAKYFPDOVFWRKPHLAVGF 417

RESULT 8  
AAB03339 ID AAB03339 standard; protein; 417 AA.

XX AAB03339;

DT 26-SEP-2000 (first entry)

XX Human RhCe protein.

XX Human, rhesus blood group system, Rh; RhD, RhCE; sickle cell disease;  
XX thalassemia; RhC, Rhc; RHE, Rhe; alloimmunisation prevention;  
XX autoimmune Rh haemolytic disease; rhesus protein; immunosuppressive;  
XX vaccine.

XX Homo sapiens.  
XX PN MO200032632-A2.  
XX

PD 08-JUN-2000.  
XX 01-DEC-1999; 99WO-GB004027.  
XX 01-DEC-1998; 98GB-00026378.  
XX (UTAB-) UNIV ABERDEEN.  
XX (COMM-) COMMON SERVICES AGENCY SCOTTISH HEALTH S.  
XX Urbanlak SJ, Barker RN;  
XX WPI; 2000-412291/35.  
XX  
XX Composition for prevention of alloimmunization or immunosuppression of a  
XX response elicited by alloimmunization or an autoimmune hemolytic disease,  
XX comprises an epitope of a rhesus protein.  
XX  
XX Disclosure; Page 85-86; 92pp; English.

CC Human blood contains the rhesus (Rh) blood group system, and humans can  
CC either be RhD positive or negative. This can lead to complications during  
CC transfusions or pregnancy if RhD negative individuals are exposed to RhD  
CC positive blood, leading to them becoming immunised to produce anti-D. The  
CC present invention relates to new human allo- and auto-reactive T-cell  
CC epitopes (AAV99760-Y99769 and AAB03201-B03337) from RhD, Rhc, Rnc, RHe  
CC and Rhe proteins. These epitopes bind to T-cells to elicit an immune  
CC response, i.e. immunisation. These epitopes can be used as a vaccine for  
CC the prevention of alloimmunisation or immunosuppression of a response  
CC elicited by alloimmunisation or an autoimmune haemolytic disease.  
CC Examples of autoimmune haemolytic diseases are sickle cell disease and  
CC thalassemia. The present sequence is the human RhCe protein from which  
CC the epitopes in the present invention were derived

SO Sequence 417 AA;

Query Match 87.5%; Score 1859; DB 3; Length 417;  
Best Local Similarity 89.9%; Pred. No. 4.2e-172; Indels 0; Gaps 0;  
Matches 375; Conservative 10; Mismatches 32;

QY 1 MSCKPRSRVORCLPLCALTLLEAAILLFFFTHYDASLEDQGLVASVYQVQDILTVMMAI 60  
DB 1 MSCKPRSRVORCLPLCALTLLEAAILLFFFTHYDASLEDQGLVASVYQVQDILTVMMAI 60  
QY 61 GIGFTTSFRRHSMSVAFNFMALGVOMAILLDGFLSOPPSGKVITLPSILATMSA 120  
DB 61 GIGFTTSFRRHSMSVAFNFMALGVOMAILLDGFLSOPPSGKVITLPSILATMSA 120  
QY 121 LSVLISVDAVIGKVNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNNMMHIYVFAAYFG 180  
DB 121 MSVLISAGAVIGKVNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNNLRHFFVFAAYFG 180  
QY 181 LTVAMCLPKPLPEGEENDDORATIPSLSAMGALFLMFRPSVNSALLRSPIERKNAVEN 240  
DB 181 LTVAMCLPKPLPEGEENDDORATIPSLSAMGALFLMFRPSVNSALLRSPIERKNAVEN 240  
QY 241 TYVAVAVSVTVAISGSSLAHPQKISMTYVHSATVLAGVAVGTSCHILPSPWLAUUGLV 300  
DB 241 TYVAVAVSVTVAISGSSLAHPQKISMTYVHSATVLAGVAVGTSCHILPSPWLAUUGLV 300  
QY 301 AGLSVRAKYLPGCCNRVIGIPHSSTINGVNFSLGLLEBITYIVLLVDTVGANGMIG 360  
DB 301 AGLSVRAKYLPGCCNRVIGIPHSSTINGVNFSLGLLEBITYIVLLVDTVGANGMIG 360  
QY 361 FOVLISIGELSLAIVIALTSGLTGLLNLKIRKAPHEAKYFPDOVFWRKPHLAVGF 417  
DB 361 FOVLISIGELSLAIVIALTSGLTGLLNLKIRKAPHEAKYFPDOVFWRKPHLAVGF 417

RESULT 9  
AAB03338 ID AAB03338 standard; protein; 417 AA.  
XX AAB03338;  
XX AC

XX	26-SEP-2000 (first entry)
DT	
XX	
DE	Human RhCE protein.
XX	
KW	Human; rhesus blood group system; Rh; RhD; RhCE; sickle cell disease;
KW	thalassaemia; Rhc; Rhd; Rhes; Rhe; alloimmunisation prevention;
KW	autoimmune Rh haemolytic disease; rhesus protein; immunosuppressive;
KW	vaccine.
XX	
OS	Homo sapiens.
XX	
PN	WO200032632-A2.
XX	
PD	08-JUN-2000.
XX	
PF	01-DEC-1999; 99WO-GB004027.
XX	
PR	01-DEC-1998; 98GB-00026378.
XX	
PA	(UTAB-) UNIV ABERDEEN.
XX	
PA	(COMM-) COMMON SERVICES AGENCY SCOTTISH HEALTH S.
XX	
PI	Urbanlak SJ, Barker RN;
XX	
DR	WPI; 2000-412291/35.
XX	
PT	Composition for prevention of alloimmunization or immunosuppression of a
PT	response elicited by alloimmunisation or an autoimmune hemolytic disease,
PT	comprises an epitope of a rhesus protein.
XX	
PS	Disclosure; Page 83-84; 92pp; English.
XX	
CC	Human blood contains the rhesus (Rh) blood group system, and humans can
CC	either be RhD positive or negative. This can lead to complications during
CC	transfusions or pregnancy if RhD negative individuals are exposed to RhD
CC	positive blood, leading to them becoming immunised to produce anti-D. The
CC	present invention relates to new human allo- and auto-reactive T-cell
CC	epitopes (AAV9760-Y99769 and AAB03201-B03337) from RhD, Rhc, Rhd, RHE
CC	and Rne proteins. These epitopes bind to T-cells to elicit an immune
CC	response, i.e. immunisation. These epitopes can be used as a vaccine for
CC	the prevention of alloimmunisation or immunosuppression of a response
CC	elicited by alloimmunisation or an autoimmune hemolytic disease.
CC	Examples of autoimmune hemolytic diseases are sickle cell disease and
CC	thalassaemia. The present sequence is the human RhCE protein from which
CC	the epitopes in the present invention were derived
XX	
XX	Sequence 417 AA;
XX	

Query Match	Similarity	87.3%	Score 1954	DB 3:	Length 417
Best Local	Similarity	89.7%	Pred. No. 1.3e-171.		
Matches	374	Conservative	10	Mismatches	33
				Indels	0
				Gaps	0
QY	1	MSCKYPRSVQRCLPLCATLTLEAAILLFYFFTHYASLEDOKGLVASYGVGGDLITVMAI	60		
		.....			
	1	MSKKPRSVRCRLPLCATLTLEAAILLFYFFTHYASLEDOKGLVASYGVGGDLITVMAI	60		
Db					
QY	61	GLGFIITSSFFRRHSWSVAFNLFMALAGVOMAILLGDLSQPSGKVITLFSITMATSA	120		
		.....			
	61	GLGFIITSSFFRRHSWSVAFNLFMALAGVOMAILLGDLSQPSGKVITLFSITMATSA	120		
Db					
QY	121	LSVLISVDVAVLGKVNLAQLVNNVLYEVTDLGNLRVYISNIENPTYHNMNMHLYVPAAYFG	180		
		.....			
	121	MSVLISAGAVLGKVNLAQLVNNVLYEVTDLGTLRWISINIPNTDYHNMNRHYVFAAYFG	180		
Db					
QY	181	LTVAACLPKPLPEGTENDNDORATIPSLSMGLGALFLAMPSPVNSALISPERKNAVEN	240		
		.....			
	181	LTVAACLPKPLPEGTENDNDORATIPSLSMGLGALFLAMPSPVNSALISPERKNAVEN	240		
Db					
QY	241	TYTAAVAVSVTAISGSSLAHPQKISKITYGHSVAVLEPEGVAVDTSCHLISPMVLPIYLGLV	300		
		.....			
	241	TYTAAVAVSVTAISGSSLAHPQKISKITYGHSVAVLEPEGVAVDTSCHLISPMVLPIYLGLV	300		
Db					

QY AGISVBRAXLYPGCCNVNVLGIPIHSSIMSGYNSSLGLLEIITYIYLVNLDYTGANGMGIG 360

DB AGLSISGAKKLPVCCNRYLGIHHHSVMHSTISLGLLEIITYIYLVNLDYTGANGMGIG 360

QY FQVLISIGELSLAIVIALTSGLLTALLNLTKIRKAPHEAKYFPDDQVFWKPHLAVGF 417

DB FQVLISIGELSLAIVIALTSGLLTALLNLTKIRKAPHEAKYFPDDQVFWKPHLAVGF 417

RESULT 10  
AAB03342  
ID AAB03342 standard; protein; 417 AA.

AC AAB03342

DT 26-SEP-2000 (first entry)

### DE Human Rhce protein.

KW Human; rhesus blood group system; Rh; RhD; RhCE; sickle cell disease.

KW autoimmune Rh haemolytic disease; rhesus protein; immunosuppressive;

XX

XX

XX

XX

XX

XX

PA (COMM-) COMMON SERVICES AGENCY SCOTTISH HEALTH S.

PI Urbanjak SJ, Barker RN;

DR WPI; 2000-412291/35.

PT Composition for prevention of alloimmunization or immunosuppression of a

PT comprises an epitope of a rhesus protein.

PS Disclosure; Page 90-92; 92pp; English.

CC Human blood contains the rhesus (Rh) blood group system, and humans can

transfusions or pregnancy if RhD negative individuals are exposed to RhD

CC present invention relates to new human allo- and auto-reactive T-cell

CC and Rhe proteins. These epitopes bind to T-cells to elicit an immune response. These epitopes can be used as a vaccine for rheumatoid arthritis.

the prevention of alloimmunisation or immunosuppression of a response

CC Examples of autoimmune haemolytic diseases are sickle cell disease and CC thalassemia. The red cell membrane is the human Rhc protein from which

CC the epitopes in the present invention were derived  
yy

SQ Sequence 417 AA;

Query Match	86.5%;	Score 1838;	DB 3;	Length 417;
Best Local Similarity	88.0%;	Prod No 4	79-170;	

Matches 371; Conservative 12; Mismatches 34; Indels 0; Gaps 0;

QY 1 MSCXPRSVQRCLPLCATLLEAALILLYFFTHYDASLEDOKGLVASYQVGQDLTVMAI 60

Db 1 MSSKYPRSVRCLPLWALTLEALILLFFFTHYDASLEDQKGLVASVQVGQDLTVMAL 60

61 GLGLTSSFRHRHSSVAFNLFMLALGVQWAILLDGLSQFPPSGKVITLFSIMLATMSA 120

Db 61 GLGFLSNFRRHSSVAFNLFMLALGVQWAILLDGFLSQPPGKVITLFSIRLATMSA 120  
 QY 121 LSVLISVDALVGKVNLAQLVWMLVEVTDLGNLRMTISINFTDYMNNMHIYVPAAYFG 180  
 Db 121 MSVLISAGAVLGKVNLAQLVWMLVEVTDLGNLRMTISINFTDYMNNMHIYVPAAYFG 180  
 QY 181 LTVAMCLPKPLPEGTEDNDQRTIPSLSAMLGALFLMFRPVSNSALLRSPTEKKAAYN 240  
 Db 181 LTVAMCLPKPLPEGTEDNDQRTIPSLSAMLGALFLMFRPVSNSALLRSPTEKKAAYN 240  
 QY 241 TYTAAVAVSVTTAISGSSLAHPQCKISKTGSHAVLPBGVAVDTSCHLIPSPMLPIVLGLV 300  
 Db 241 TYTAAVAVSVTTAISGSSLAHPQCKISKTGSHAVLPBGVAVDTSCHLIPSPMLPIVLGLV 300  
 QY 301 AGLISVRGAKYLPGCCNRVLGIPIHSSIMGVNFSLLGLEIYIYVLVDTVGAGNGMIG 360  
 Db 301 AGLISGAKCLPVCNRLVGIHHSIVMHSIFSLGLGLEIYIYVLVDTVGAGNGMIG 360  
 QY 361 FOVLISIGLSLAIVALTSGLLTLLNLKIRKAPHEAKYFDDQVFWKFPHLAVGF 417  
 Db 361 FOVLISIGLSLAIVALTSGLLTLLNLKIRKAPHEAKYFDDQVFWKFPHLAVGF 417

## RESULT 11

AAB03340

ID AAB03340 standard; protein; 417 AA.

AC AAB03340;

DT 26-SEP-2000 (first entry)

DE Human Rhce protein.

KM Human; rhesus blood group system; Rh; Rnd; Rhce; sickle cell disease;  
 KW thalassemia; Rhc; Rhg; Rhe; alloimmunisation prevention;  
 KW autoimmune Rh haemolytic disease; rhesus protein; immunosuppressive;  
 vaccine.

OS Homo sapiens.

PN WO200032632-A2.

PD 08-JUN-2000.

PF 01-DEC-1999; 99WO-GB004027.

PR 01-DEC-1998; 98GB-00026378.

PA (UYAB-) UNIV ABERDEEN.

PA (COMM-) COMMON SERVICES AGENCY SCOTTISH HEALTH S.

PI Urbanlak SJ, Barker RN;

DR WPI; 2000-412291/35.

FT Composition for prevention of alloimmunization or immunosuppression of a  
 PT response elicited by alloimmunization or an autoimmune hemolytic disease,  
 PT comprises an epitope of a rhesus protein.

PS Disclosure; Page 86-88; 92pp; English.

CC Human blood contains the rhesus (Rh) blood group system, and humans can  
 CC either be RhD positive or negative. This can lead to complications during  
 CC transfusions or pregnancy if RhD negative individuals are exposed to RhD  
 CC positive blood, leading to them becoming immunised to produce anti-D. The  
 CC present invention relates to new human allo- and auto-reactive T-cell  
 CC epitopes (AAV99760-Y99769 and AAB03201-B03337) from RhD, Rhc, Rhd, RHE  
 CC and Rne proteins. These epitopes bind to T-cells to elicit an immune  
 CC response, i.e. immunisation. These epitopes can be used as a vaccine for  
 CC the prevention of alloimmunisation or immunosuppression of a response  
 CC elicited by alloimmunisation or an autoimmune hemolytic disease.  
 CC Examples of autoimmune hemolytic diseases are sickle cell disease and  
 CC thalassemia. The present sequence is the human Rhce protein from which

CC the epitopes in the present invention were derived  
 XX SQ Sequence 417 AA;

Query Match 86.3%; Score 1833; DB 3; Length 417;  
 Best Local Similarity 98.7%; Pred. No. 1,4e-169;  
 Matches 370; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

QY 1 MSCKYPSVORCLPLCALTEALILLFYPTHYDASLEDQKGVASVGVGDLTWMAAI 60  
 Db 1 MSCKYPSVORCLPLCALTEALILLFYPTHYDASLEDQKGVASVGVGDLTWMAAI 60  
 QY 61 GLGFLSNFRRHSSVAFNLFMLALGVQWAILLDGFLSQPPGKVITLFSIRLATMSA 120  
 Db 61 GLGFLSNFRRHSSVAFNLFMLALGVQWAILLDGFLSQPPGKVITLFSIRLATMSA 120  
 QY 121 LSVLISVDALVGKVNLAQLVWMLVEVTDLGNLRMTISINFTDYMNNMHIYVPAAYFG 180  
 Db 121 MSVLISAGAVLGKVNLAQLVWMLVEVTDLGNLRMTISINFTDYMNNMHIYVPAAYFG 180  
 QY 181 LTVAMCLPKPLPEGTEDNDQRTIPSLSAMLGALFLMFRPVSNSALLRSPTEKKAAYN 240  
 Db 181 LTVAMCLPKPLPEGTEDNDQRTIPSLSAMLGALFLMFRPVSNSALLRSPTEKKAAYN 240  
 QY 241 TYTAAVAVSVTTAISGSSLAHPQCKISKTGSHAVLPBGVAVDTSCHLIPSPMLPIVLGLV 300  
 Db 241 TYTAAVAVSVTTAISGSSLAHPQCKISKTGSHAVLPBGVAVDTSCHLIPSPMLPIVLGLV 300  
 QY 301 AGLISVRGAKYLPGCCNRVLGIPIHSSIMGVNFSLLGLEIYIYVLVDTVGAGNGMIG 360  
 Db 301 AGLISGAKCLPVCNRLVGIHHSIVMHSIFSLGLGLEIYIYVLVDTVGAGNGMIG 360  
 QY 361 FOVLISIGLSLAIVALTSGLLTLLNLKIRKAPHEAKYFDDQVFWKFPHLAVGF 417  
 Db 361 FOVLISIGLSLAIVALTSGLLTLLNLKIRKAPHEAKYFDDQVFWKFPHLAVGF 417

## RESULT 12

ADR09337

ID ADR09337 standard; protein; 401 AA.

AC ADR09337;

DT 04-NOV-2004 (first entry)

DE Human protein useful for treating neurological disease Seq 2843.

KM human; oligo-capping method; diagnostic marker; gene therapy;  
 KW osteoporosis; neurological disease; Alzheimer's disease;  
 KW Parkinson's disease; dementia; short memory; cancer;  
 KW sense or motor function; emotional reaction; fear response; panic;  
 KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cyostatic;  
 KW tranquiliser.

OS Homo sapiens.

PN EPI447413-A2.

PD 18-AUG-2004.

PF 12-FEB-2004; 2004EP-00003145.

PR 14-FEB-2003; 2003JP-00102207.

PR 09-MAY-2003; 2003JP-00131452.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

PI Isogai T, Yamamoto J, Nishikawa T, Isomo Y, Sugiyama T, Otsuki T;

PI Wakamatsu A, Ishii S, Nagai K, Irie R;

DR WPI; 2004-583265/57.

XX N-PSDB; ADR07381.

PT New 1995 CDNA, useful for treating osteoporosis, neurological diseases,  
PT Alzheimer's diseases, Parkinson's disease, dementia and various cancers  
XX  
PS Claim 1, SEQ ID NO 2843, 2686pp; English.

CC This invention relates to novel, isolated full length human cDNA  
CC molecules and the encoded proteins thereof. Specifically, it refers to  
CC cDNA clones obtained by an oligo-capping method, where none of these  
CC clones are identical to any known human mRNAs. The present invention  
CC describes an immunoassay to identify agonists and antagonists, as well as  
CC antibodies, antisense molecules and siRNAs that can all be used to bind  
CC to and modulate expression of the cDNA molecules. As such, these  
CC molecules are useful for diagnostic markers or therapeutic targets for  
CC the various diseases or morbid states, in particular they are useful in  
CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's  
CC disease, Parkinson's disease, dementia, short memory and various cancers,  
CC as well as for maintaining equilibrium of sense or motor function, and  
CC for treating emotional reaction, fear response and panic. Accordingly,  
CC they exhibit osteoprotactic, neuroprotective, nociceptive, antiparkinsonian,  
CC cytosarctic and tranquilliser activities. This polypeptide is a protein  
CC encoded by a full length human cDNA sequence of the invention. NOTE: This  
CC sequence is not given in the sequence listing of the specification but  
CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-  
CC office.

**SQ Sequence 401 AA;**

Query Match	75.6%	Score 1605	DB 8	Length 401
Best Local Similarity	98.0%	Pred. No. 2.2e-147		
Matches 324	Conservative 11	Mismatches 33	Indels 0	Gaps 0

[illegible]

RESULT 13  
ADD46523  
ID ADD46523 standard; protein; 422 AA

AC ADD46523 ;

DT 02-DEC-2004 (revised)

DT 29-JAN-2004 (first entry)

DE Rat Protein NP\_071950, SEQ ID NO 12204.

KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX	
OS	Rattus norvegicus.
OS	Unidentified.

PN WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GEHO ) GEN HOSPITAL CORP.

LEADS / BATES NO:  
XX  
XX

FI MOULT C, DUBBO D, BEZOLC N, COBOLGIAN M, XY

DK WPT; 2003-268312/26  
DB GENBANK; MB 071950

XX  
XX  
XX

preparing a medicam

PS Example 1; Page; 1017pp; English.

CC The invention discloses a composition

CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (described in Table 3  
CC of the specification) which is differentially expressed during pain.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPD at  
CC ftp.wipd.int/pub/published\_pct\_sequences.

**SQ** Sequence 422 AA

Query Match	46.7%	Score 991.5	DB 7	Length 422
Best Local Similarly	52.1%	Pred. No. 1.4e-87		
Matches 222	54	Mismatches 137	Indels 13	Gaps 5

QY 1 MSCKYPRSVQRCPLPCALTLEALILLFYFTHYDASLEDQGLVASVQVGODLTWMAI 60

db 1 MGSKYPRSLRCLPLWAFGLQVTFILLFYFLIGQDPIDADHK-FMAIYQVIQDLTLVAAL 59

Qy 61 GLGFLTSSFRHSSVAFNLEMLALGVQWAILLDGFLSQFPSCKVITLPSIML---A 1166



QY 177 AYFGITVAMCLPKPREGEDND-----QRATIPSLAMGLFLMFRPSVNSALLRSP 231  
 DB 180 AYFGITVAMVLSKSLPRRHHNQTEKVQMTTSSLPAMGLTFLMFWPINSALLRG- 238  
 QY 232 IERKNAVENTYYAVAVSVTAISGSSLAHPQKISKTYGHSAYLPBGAVDTSCHLIPSP 291  
 DB 239 TKKNAVENTYYAALAVSTVATSMASLSHPKKNVHINNAVLAGVAVGAPSCLISSP 298  
 QY 292 MLPYVLGLVAGLISVRGAKYLPCCNRYLGIPIHSSIMGYNFSLGLEETIYVLVLDLT 351  
 DB 299 WIMAVGLTAGLISIWGAKCPQVCLSDLLNP--SGIHFTFGLGLGLATYYCHITAE 356  
 QY 352 VGAGNGMIGFOVLTISGELSLAIVALTSGLLTALLNLKIRKAPHEAKYFDDQVFWKFP 411  
 DB 357 SRPSNLMIVTQITTDVGLSPFAMAMGMVTLTGCLLSVKWRAPHAVKYFPDQAFWFRP 416  
 QY 412 HLAVER 417  
 DB 417 HLAVER 422

RESULT 14  
 ADE54447  
 ID ADE54447 standard; protein; 422 AA.  
 XX

AC ADE54447;  
 XX  
 DT 29-JAN-2004 (first entry)  
 DE Rat Protein NP\_071950, SEQ ID NO 250.

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
 OS Rattus norvegicus.

PN WO2003016475-A2.

PD 27-FEB-2003.

PP 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GENO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI Woolf C, D'Urso D, ReFort K, Costigan M;

DR WPI; 2003-268312/26.

DR GENBANK; NP\_071950.

PT New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

PS Claim 1; Page; 1017p; English.

XX The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying a pain and a  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPD at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 422 AA;

Query Match 46.7%; Score 991.5; DB 7; Length 422;  
 Best Local Similarity 52.1%; Pred. No. 1,4e-87;  
 Matches 222; Conservative 54; Mismatches 137; Indels 13; Gaps 5;

QY 1 MSCKYPRSVQRCLPLCALTLLEALILFFFTHYDASLEDOKGLVASYGVODLTVMAAI 60

DB 1 MGSKYPRSLRCLPLWAFGLQVTFILLFYELIGQDPIQADHK-FMAIVGIQDITLVNAL 59

QY 61 GLGFLTSPRRHSVAFNLFWALAGVOMAILDGLSOFPSGKVITLSEIWL----A 116

DB 60 GFGFLSSRRHGWSSVAFSFMALAGVGTILLFYLMVLDMMNINPFSPLIGRA 119

QY 117 TMSALSVLISVDVAGLKVLAQLVVAVLEVDLGNLKVISINFTDVMHMMHIIYFA 176

DB 120 TISTLEPLISAGAVLGKVLQVAVVLEANTPFAIVADKVRIDHIIMTGHWFG 179

QY 177 AYFGITVAMCLPKPREGEDND-----QRATIPSLAMGLFLMFRPSVNSALLRSP 231

DB 180 AYFGITVAMVLSKSLPRRHHNQTEKVQMTTSSLPAMGLTFLMFWPINSALLRG- 238

QY 232 IERKNAVENTYYAVAVSVTAISGSSLAHPQKISKTYGHSAYLPBGAVDTSCHLIPSP 291

DB 239 TKKNAVENTYYAALAVSTVATSMASLSHPKKNVHINNAVLAGVAVGAPSCLISSP 298

QY 292 MLPYVLGLVAGLISVRGAKYLPCCNRYLGIPIHSSIMGYNFSLGLEETIYVLVLDLT 351

DB 299 WIMAVGLTAGLISIWGAKCPQVCLSDLLNP--SGIHFTFGLGLGLATYYCHITAE 356

QY 352 VGAGNGMIGFOVLTISGELSLAIVALTSGLLTALLNLKIRKAPHEAKYFDDQVFWKFP 411

DB 357 SRPSNLMIVTQITTDVGLSPFAMAMGMVTLTGCLLSVKWRAPHAVKYFPDQAFWFRP 416

QY 412 HLAVER 417

DB 417 HLAVER 422

RESULT 15

ADE54443  
 ID ADE54443 standard; protein; 422 AA.

AC ADE54443;  
 XX

DT 29-JAN-2004 (first entry)

DE Rat Protein NP\_071950, SEQ ID NO 246.

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

OS Rattus norvegicus.

PN WO2003016475-A2.

PD 27-FEB-2003.

PP 14-AUG-2002; 2002WO-US025765.



XX 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX MPI; 2003-268312/26.  
DR GENBANK; NP\_071950.  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
preparing a medicament for treating pain in an animal.  
XX  
PS Claim 1; Page; 1017p; English.  
XX  
CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX  
SQ Sequence 422 AA;  
  
Query Match 46.7%; Score 991.5; DB 7; Length 422;  
Best Local Similarity 52.1%; Pred. No. 1,4e-87;  
Matches 222; Conservative 54; Mismatches 137; Indels 13; Gaps 5;  
  
QY 1 MSCKYPRSVQRCLPLCALTEALILLFPFTHYDASLEDOKGLVASVYOGDITVMAAI 60  
DB 1 MGSKYPRSLRCLPLMAFGLOVTFILFVFLIGQDPHQADHK-FMALYQVIODLTVAAAL 59  
  
QY 61 GLGFLTSSFRHSSSVAFNLFMALGVQNALILDGFLSQFPGSKVYITLFSITWL---A 116  
DB 60 GFGFLSSFRHSSSVAFNLFMALGVQNTLLDYLFWLDMWNMIKNPSPFLSIQRA 119  
  
QY 117 TMSALSVLISVDAVLGKNTLAQLVVMVLVEVTDGNLRMTVINSIFNTDYHNNMHHIVFA 176  
DB 120 TISTPLPLISAGAVLGKVNVLQALVMVLVEAMTFGAIRVADKKVFRIEDHIIMYGHVFG 179  
  
QY 177 AYFGLTVAMCLPKPLPEGTEDND----QRATIPSLSAMLGALFLMMFRPSVNSALLRSP 231  
DB 180 AYFGLTVAMWLSKSLPRRRHENAQTEKVKQMTSSSLFAMLGTLFLMIFWPSINSALLRG- 238  
  
QY 232 IERRNAVENTYVAVSVMTAAGSSSLAHQGRKSKTYGSAVLPBGVAVDTSCHLPSF 291  
DB 239 TKKNAVENTYVAVSVMTAAGSSSLAHQGRKSKTYGSAVLPBGVAVDTSCHLPSF 298  
  
QY 292 WLPVIVGLVAGLISVRGAKYLPGCCNRVLGI PHSSIMGYNFSLGLLEETIYIVLVLDIT 351

DB 299 WIMVVLGTAGLISIMGAKCPQVCLSDLLNP---SGIHYTFGLRGULGALTYCTHIIAE 356  
QY 352 VGANGMIGQVQLSTIGELSLAIVIALTSGLLRALLNLKIRKAPHEAKTFDDQVFWKFP 411  
DB 357 SRPSNLWIVQTITDVGALSPAMAMGVTLTGCLLSVYKWRAPHAVKYFDDQAFWEFP 416  
QY 412 HLAVER 417  
DB 417 HLAVER 422

Search completed: March 24, 2005, 13:16:41  
Job time : 168 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 24, 2005, 13:17:10 ; Search time 142 Seconds  
(without alignments)  
972.317 Million cell updates/sec

Title: CAC07879  
Perfect score: 2124  
Sequence: 1 MSCKYRSVGRCLPLCALTL.....EAKYFDQVWKPFLAVGF 417

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues  
Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB.pep:\*  
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20: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	* Query Match Length	ID	Description
1	521	24.5	459 15 US-10-074-978A-246	Sequence 246, App
2	497	23.4	479 9 US-09-949-145-3	Sequence 3, Appl
3	497	23.4	479 15 US-10-074-978A-244	Sequence 244, App
4	490	23.1	445 15 US-10-074-978A-42	Sequence 42, Appl
5	488.5	23.0	498 9 US-09-949-145-4	Sequence 4, Appl
6	488.5	23.0	498 15 US-10-074-978A-245	Sequence 245, App
7	486	22.9	467 15 US-10-074-978A-247	Sequence 247, App
8	480.5	22.6	455 15 US-10-190-115-58	Sequence 58, Appl
9	480.5	22.6	455 15 US-10-369-072-58	Sequence 59, Appl
10	477	22.5	458 15 US-10-190-115-59	Sequence 59, Appl
11	477	22.5	458 15 US-10-369-072-59	Sequence 59, Appl
12	476	22.4	324 16 US-10-408-765A-1089	Sequence 1089, Ap
13	472.5	22.2	458 15 US-10-190-115-57	Sequence 57, Appl

14	472.5	22.2	458 15 US-10-369-072-57	Sequence 57, Appl
15	466.5	22.0	458 15 US-10-190-115-55	Sequence 55, Appl
16	466.5	22.0	458 15 US-10-369-072-55	Sequence 55, Appl
17	465.5	21.9	458 15 US-10-190-115-56	Sequence 56, Appl
18	465.5	21.9	458 15 US-10-369-072-56	Sequence 56, Appl
19	464	21.8	458 15 US-10-074-978A-248	Sequence 248, Appl
20	444	20.9	458 15 US-10-074-978A-249	Sequence 249, Appl
21	374	17.6	448 15 US-10-190-115-22	Sequence 22, Appl
22	374	17.6	448 15 US-10-369-072-22	Sequence 22, Appl
23	302	14.2	366 15 US-10-264-237-2412	Sequence 2412, Ap
24	257	12.1	54 9 US-09-864-761-34840	Sequence 34840, A
25	247.5	11.7	395 15 US-10-190-115-100	Sequence 100, App
26	247.5	11.7	395 15 US-10-369-072-100	Sequence 100, App
27	220	10.4	373 15 US-10-074-978A-250	Sequence 250, App
28	202	9.5	145 14 US-10-012-548-438	Sequence 438, App
29	202	9.5	145 14 US-10-115-123-438	Sequence 438, App
30	164.5	7.7	459 9 US-09-795-693-32	Sequence 32, Appl
31	164.5	7.7	459 14 US-10-156-233-32	Sequence 32, Appl
32	164.5	7.7	459 14 US-10-199-485-32	Sequence 32, Appl
33	142	6.7	308 14 US-10-012-548-437	Sequence 437, App
34	142	6.7	308 14 US-10-115-123-437	Sequence 437, App
35	124.5	5.9	447 15 US-10-282-122A-52221	Sequence 52221, A
36	122	5.7	523 15 US-10-282-122A-52841	Sequence 62841, A
37	120	5.6	66 11 US-09-864-408A-1672	Sequence 1672, Ap
38	120	5.6	537 15 US-10-282-122A-64691	Sequence 64691, A
39	119.5	5.6	424 15 US-10-369-493-1146	Sequence 1146, Ap
40	119.5	5.6	891 15 US-10-282-122A-77590	Sequence 77590, A
41	117.5	5.5	612 15 US-10-282-122A-58936	Sequence 58936, A
42	114	5.4	529 14 US-10-156-761-12058	Sequence 12058, A
43	114	5.4	801 15 US-10-282-122A-70493	Sequence 70493, A
44	113.5	5.3	440 15 US-10-282-122A-59941	Sequence 59941, A
45	113.5	5.3	601 15 US-10-369-493-11844	Sequence 11844, A

#### ALIGNMENTS

RESULT 1  
US-10-074-978A-246  
; Sequence 246, Application US/10074978A  
; Publication No. US20040010119A1  
; GENERAL INFORMATION:  
; APPLICANT: Leite, Mario  
; APPLICANT: Spytek, Kimberly A  
; APPLICANT: Guo, Xiaojia (Sasha)  
; APPLICANT: Fernandes, Elma  
; APPLICANT: Li, Li  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Casman, Stacie  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Patuturajan, Meera  
; APPLICANT: Bialock, Angela  
; APPLICANT: Ballinger, Robert  
; APPLICANT: Vernet, Corine  
; APPLICANT: Tchernev, Velizar T  
; APPLICANT: Malynkar, Uriel M  
; APPLICANT: Gusev, Vladimir  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Mezes, Peter S  
; APPLICANT: Ellerman, Karen  
; APPLICANT: Hayes, Melvin P  
; APPLICANT: Herman, John  
; APPLICANT: Pena, Carol E A  
; APPLICANT: Shinkete, Richard A  
; APPLICANT: Taupier Jr, Raymond J  
; APPLICANT: Moore, No. US20040010119A111e  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Edinger, Shlomit  
; APPLICANT: Gunther, Erik  
; APPLICANT: Stone, Dave  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Peyman, John

```

; APPLICANT: Smithsonian, Glenda
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269
; CURRENT APPLICATION NUMBER: US/10/074, 978A
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268, 221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335, 109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312, 284
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268, 496
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/276, 703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330, 293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322, 127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280, 899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310, 797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268, 646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 246
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-074-978A-246

Query Match
Best Local Similarity 24.5%; Score 521; DB 15; Length 459;
Matches 138; Conservative 75; Mismatches 177; Indels 48; Gaps 10;

13 LPLCALTEALILFFFTHYDASLED---OKGLVAS-----YVGQDUTVM 57
11 LPLVALLVALLLFGVFRYDMDADPHWQEKVIXLSTDLNEFEYRPSFQDVHM 70
58 AALGGLTSSFRHSSVAENLFLALGVQWAILLDGFLSOPPSKVVITLFSITLAT 117
71 IFVGFGLMTFLQRYGSSVGFN-FLAAGIQWALLMQWLGOSDGRYIIVDLNLINAD 129
118 MSALSVLSVAVYKVNLAQLVVWVLEVTDLGNLRMVISNIFNTDYHNMNHIYVFAA 177
130 FCVGSVCVAFGAVIGKVSPOVLLIMTLFQVTLFSEINEXIILLNLEVDGSGSMTHAFGA 189
178 YFGITVAMCPEKPLPEGEDNDQKATIPSLSAMIGALFLMFRPSVNSALRSPIERKVA 237
190 YFGITVAMILYRPMUHSKESQSTYHSDLPAMIGTLFLMWYSPFNSAISNHGDAQHRA 249
238 VENTYVAVAVSVTAISGSSLAHPQKISKTYGSAVLPEGVAVDTSCHLIPSPMLPIYL 297
250 AINYYCSIAACVLTSSALHKKGLDMVHIQNMTLAGSVGLYAEIMLVIPFSSLTI 309
298 GLVAGLISVGAAYL-----PGCCNRYLGIPIHSSIMGVNFSLL 335
310 GFVGVISTLGFVYLLPFLESRLHIQDTGCVNHLHGIPGIIIGIAGAVASIA--NIDLY 367
336 GLLEELIYIVLVLDVYAGNMGIG-FQVLLSIGELISALIVALTSGILTALLNLTKI-R 393
368 G-EEGLAVAFGIRSKLMSPNNOGRFQA---AGLFSILMALVGVIVGVILRLPFWG 422
394 KAPHEAKYFPDOVFWKFP 411
423 QAPDE-NCEPDVAYWEIP 439

RESULT 2
US-09-949-145-3
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; Sequence 3, Application US/09949145
; Patent No. US20020055622A1
; GENERAL INFORMATION:
; APPLICANT: New York Blood Center
; TITLE OF INVENTION: Mammalian No. US20020055622A1-erythroid Rh Type C Genes and Glycoi
; FILE REFERENCE: Docket 454-31
; CURRENT APPLICATION NUMBER: US/09/949, 145
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/230660
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 3
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-949-145-3

Query Match
Best Local Similarity 23.4%; Score 497; DB 9; Length 479;
Matches 129; Conservative 77; Mismatches 183; Indels 50; Gaps 8;

13 LPLCALTEALILFFFTHYD-----ASLEDKG-LVASVYQGDUTVMA 58
11 LPLTCLLVIVIVILFGVFRYDDEADAHMSEKTHKNSDNEFEYRPSFQDVHMV 70
59 AALGGLTSSFRHSSVAENLFLALGVQWAILLDGFLSOPPSKVVITLFSITLATM 118
71 FVGFGLMTFLQRYGSSVGFN-FLAAGIQWALLMQWLGOSDGRYIIVDLNLINAD 130
119 SALSVLSVDAVLGKVNLAQLVVWVLEVTDLGNLRMVISNIFNTDYHNMNHIYVFAAY 178
131 CVASVCVAFGAVIGKVSPOVLLIMTLFQVTLFVAVNEFLILNLKVKDAGSGMTHTTFCAY 190
179 FGLTVAMCPEKPLPEGEDNDQKATIPSLSAMIGALFLMFRPSVNSALRSPIERKVA 238
191 FGLTVRILYRNLHQSKEQNSVYQSDLPAMIGTLFLMWYSPFNSAISNHGDAQHRA 250
239 FNTYVAVAVSVTAISGSSLAHPQKISKTYGSAVLPEGVAVDTSCHLIPSPMLPIYL 298
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299 LVAGLISVGAAYL-----PGCC--NRVLGIPIHSSIMGVNFSLLGLEELIYIVL 346
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393 KAPHEAKYFPDOVFWKFP 411
421 WQSPDENCFEDVAYWEIP 439

RESULT 3
US-10-074-978A-244
; Sequence 244, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiaohong
; APPLICANT: Caeman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patuturajan, Meera
; APPLICANT: Blalock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corinne
```

```
/ APPLICANT: Tchernev, Velizar T
/ APPLICANT: Malyankar, Uriel M
/ APPLICANT: Gusev, Vladimir
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Mezes, Peter S
/ APPLICANT: Ellerman, Karen
/ APPLICANT: Heyes, Melvin P
/ APPLICANT: Herrman, John
/ APPLICANT: Pena, Carol E A
/ APPLICANT: Shinkete, Richard A
/ APPLICANT: Taupier Jr, Raymond J
/ APPLICANT: Moore, No. US20040010119A11le
/ APPLICANT: Shenoy, Suresh
/ APPLICANT: Edinger, Shlomit
/ APPLICANT: Gunther, Erik
/ APPLICANT: Stone, Dave
/ APPLICANT: Millet, Isabelle
/ APPLICANT: Peyman, John
/ APPLICANT: Smlthson, Glenda
/ TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 21402-269
/ CURRENT APPLICATION NUMBER: US/10/074,978A
/ CURRENT FILING DATE: 2003-01-07
/ PRIOR APPLICATION NUMBER: 60/268,221
/ PRIOR FILING DATE: 2001-02-12
/ PRIOR APPLICATION NUMBER: 60/335,109
/ PRIOR FILING DATE: 2001-10-31
/ PRIOR APPLICATION NUMBER: 60/312,284
/ PRIOR FILING DATE: 2001-08-14
/ PRIOR APPLICATION NUMBER: 60/268,496
/ PRIOR FILING DATE: 2001-02-13
/ PRIOR APPLICATION NUMBER: 60/276,703
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/330,293
/ PRIOR FILING DATE: 2001-10-18
/ PRIOR APPLICATION NUMBER: 60/322,127
/ PRIOR FILING DATE: 2001-11-21
/ PRIOR APPLICATION NUMBER: 60/280,899
/ PRIOR FILING DATE: 2001-04-02
/ PRIOR APPLICATION NUMBER: 60/310,797
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: 60/268,646
/ PRIOR FILING DATE: 2001-02-14
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 547
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 244
/ LENGTH: 479
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-074-978A-244

Query Match      23.4%; Score 497; DB 15; Length 479;
Best Local Similarity 29.4%; Pred. No. 1,36-37;
Matches 129; Conservative 77; Mismatches 183; Indels 50; Gaps 8;
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Qy      347 LVLDIVGAGNGMT-----GF-----QVLSIGELSLAIVIALTSGLLTALLNLKI 392
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Db      421 WQGPSPDNCEDADAVWEMP 439

RESULT 4
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/ Sequence 42, Application US/10074978A
/ Publication No. US20040010119A1
/ GENERAL INFORMATION:
/ APPLICANT: Leite, Mario
/ APPLICANT: Spytek, Kimberly A
/ APPLICANT: Guo, Xiaojia (Sasha)
/ APPLICANT: Fernandes, Elma
/ APPLICANT: Li, Li
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Liu, Xiaohong
/ APPLICANT: Casman, Stacie
/ APPLICANT: Boldog, Ferenc
/ APPLICANT: Patuvarajan, Meera
/ APPLICANT: Bialock, Angela
/ APPLICANT: Ballinger, Robert
/ APPLICANT: Verneil, Corine
/ APPLICANT: Tchernev, Velizar T
/ APPLICANT: Malyankar, Uriel M
/ APPLICANT: Gusev, Vladimir
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Mezes, Peter S
/ APPLICANT: Ellerman, Karen
/ APPLICANT: Heyes, Melvin P
/ APPLICANT: Herrman, John
/ APPLICANT: Pena, Carol E A
/ APPLICANT: Shinkete, Richard A
/ APPLICANT: Taupier Jr, Raymond J
/ APPLICANT: Moore, No. US20040010119A11le
/ APPLICANT: Shenoy, Suresh
/ APPLICANT: Edinger, Shlomit
/ APPLICANT: Gunther, Erik
/ APPLICANT: Stone, Dave
/ APPLICANT: Millet, Isabelle
/ APPLICANT: Peyman, John
/ APPLICANT: Smlthson, Glenda
/ TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 21402-269
/ CURRENT APPLICATION NUMBER: US/10/074,978A
/ CURRENT FILING DATE: 2003-01-07
/ PRIOR APPLICATION NUMBER: 60/268,221
/ PRIOR FILING DATE: 2001-02-12
/ PRIOR APPLICATION NUMBER: 60/335,109
/ PRIOR FILING DATE: 2001-10-31
/ PRIOR APPLICATION NUMBER: 60/312,284
/ PRIOR FILING DATE: 2001-08-14
/ PRIOR APPLICATION NUMBER: 60/268,496
/ PRIOR FILING DATE: 2001-02-13
/ PRIOR APPLICATION NUMBER: 60/276,703
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/330,293
/ PRIOR FILING DATE: 2001-10-18
/ PRIOR APPLICATION NUMBER: 60/322,127
/ PRIOR FILING DATE: 2001-11-21
/ PRIOR APPLICATION NUMBER: 60/280,899
/ PRIOR FILING DATE: 2001-04-02
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; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 42
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-074-978A-42

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Query Match      23.1%; Score 490; DB 15; Length 445;
Best Local Similarity 29.3%; Pred. No. 5,5e-37;
Matches 128; Conservative 77; Mismatches 182; Indels 50; Gaps 8;

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DB 71 FVGFGLMTFLQRYGSAVGFNPLAARFQIALMKGFMHFLQDRYIVGVENLINDF 130
QY 119 SALSVLISVDAYLCKNLAQLVVMVLVEYTDLGNLRMVISNIFNTDYHNNMHIYVFAAY 178
DB 131 CAASVCVAGAVLGVKSPQLIMTFEYVTLFVAVNEFILNLKPKDAGSGMTIHTFCAY 190
QY 179 FGLTVAMCLPKPLPEGTEDNDQRATIPSLAMLGALFLMPPSPNSALLSPERKNAV 238
DB 191 FGLTVIRILYRNLDQSKRQNSVYQSDLFAMIGTLFIMTWPSFNSAISYHGDSDHRAA 250
QY 239 FNTTYAVAVSVTAISGSLAHPOGKISKTYGSAVLPEGVAVDTSCHLIPSPMLPYLG 298
DB 251 INTYGSILACVLTVAISSALHKKGLDMVHIQNTLAGVAVGAEMMLTPGALIIIG 310
QY 299 LVAGLISVGAAYL-----PGCC--NRVLGIPHSIMGNISLGLLEIYIVL 346
DB 311 FVCGIISTLGFVYTLFPLESRRLHIDTCGINNHGIP-----GIIGIVGAVTAAS 361
QY 347 LVLDTVGANGMI-----GF-----QVLLSIGELSLAIVALTSGLLTALLNLKI 392
DB 362 ASLEVYGR-EGLVHSFDFQGFNGDMTARTQCKPQIYGLVTLAMALMGIIIVGLILKLP 420
QY 393 RKAPHEAKYEDDOYFWK 409
DB 421 WGPSDENCEFEDAVYWE 437

```

```

RESULT 5
US-09-949-145-4
; Sequence 4, Application US/09949145
; Patent No. US20020055622A1
; GENERAL INFORMATION:
; APPLICANT: New York Blood Center
; TITLE OF INVENTION: Mammalian No. US20020055622A1-erythroid Rh Type C Genes and Glyco
; FILE REFERENCE: Docket 454-31
; CURRENT APPLICATION NUMBER: US/09/949,145
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/230660
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 4
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-949-145-4

```

```

Query Match      23.0%; Score 488.5; DB 9; Length 498;
Best Local Similarity 28.0%; Pred. No. 8,9e-37;
Matches 120; Conservative 86; Mismatches 191; Indels 31; Gaps 4;

```

```

QY 13 LPLCALTEALLLFFFTHYDAS-----LEDQKGLVAS-----YQVGDLTVM 57
DB 11 LPLTCLLOVIMVILFVGFRYDDIQAADAHMWELEKRNKISSDVWENEFYRPSFQDVHVM 70
QY 58 AIGLGLTSSFRHSWSVAFLFMLALGVMAIILDGFLSQFPGKVIITLFSIWLAT 117
DB 71 FVGFGLMTFLQRYGSAVGFNPLAARFQIALMKGFMHFLQDRYIVGVENLIND 130
QY 118 MSALSVLISVDAYLCKNLAQLVVMVLVEYTDLGNLRMVISNIFNTDYHNNMHIYVFAA 177
DB 131 FCVASSCVAGAVLGVKSPQQLIMTFEYVTLFVAVNEFILNLKPKDAGSGMTIHTFCA 190
QY 178 FGLTVAMCLPKPLPEGTEDNDQRATIPSLAMLGALFLMPPSPNSALLSPERKNA 237
DB 191 FGLTVIRILYRNLDQSKRQNSVYHSDLFAMIGTLFIMTWPSFNSASHGDHRA 250
QY 238 FNTTYAVAVSVTAISGSLAHPOGKISKTYGSAVLPEGVAVDTSCHLIPSPMLPYL 297
DB 251 ALNTYLSLASVLTVTVAISSIVHKKGLDMVHIQNTLAGVAVGAEMMLTPGALIIY 310
QY 298 GLVAGLISVGAAYLPGCCNRVLGIPHSIMGNISLGLLEIYIVL----- 347
DB 311 GFPCGIFSTLGFAYTLFPLESRRLHIDTCGINNHGIPETIGIVGAVTAAYSSPDYGE 370
QY 348 --VLDTVAGANGMIGF---QVLLSIGELSLAIVALTSGLLTALLNLKIRKAPHEAKY 401
DB 371 FGLTVIRILYRNLDQSKRQNSVYHSDLFAMIGTLFIMTWPSFNSASHGDHRA 430
QY 402 FDDOVPFWK 409
DB 431 FEDSTIYWE 438

```

```

RESULT 6
US-10-074-978A-245
; Sequence 245, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiaohong
; APPLICANT: Casman, Stacie
; APPLICANT: Boleog, Ferenc
; APPLICANT: Paturajan, Meera
; APPLICANT: Blalock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Verner, Corine
; APPLICANT: Tcherenev, Velizar T
; APPLICANT: Maljankar, Uriel M
; APPLICANT: Gusev, Vladimyr
; APPLICANT: Raetelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Herrman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shinkets, Richard A
; APPLICANT: Tauplier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A111e
; APPLICANT: Shenoy, Suresh
; APPLICANT: Edinger, Shiomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269

```

```

; CURRENT APPLICATION NUMBER: US/10/074,978A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268,221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335,109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312,284
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268,496
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/276,703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330,293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322,127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280,899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 245
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-074-978A-245
```

```

Query Match      23.0%; Score 488.5; DB 15; Length 498;
Best Local Similarity 28.0%; Pred. No. 8.9e-37;
Matches 120; Conservative 86; Mismatches 191; Indels 31; Gaps 4;
```

```

QY 13 LPLCALTLLEAALLLFFFTTHYDAS-----LEDOKGLVAS-----YVGQDLTVM 57
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 11 LPLTCLLYQTMVVLFGVFRYDIQADAHMMLLEKKRKNISDVENEFRYRPSQDVHAM 70
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 58 AAIIGLGLTSSFRHRSNVAENLPMALGVQMAILLDGLSQFPSPGKVVITLFSYLAT 117
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 71 VPGVFGFLMTFLQRYGFSAVGFNLLAFCGIOMALLMGWFHYPEEGHIVLSVENIIOAD 130
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 118 MSALSVLISVDAYLCKNLQOLVVMVLVEVTDGLNLMVSNIENTYHNMWHIYVEAA 177
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 131 FCVAASCVAAFGAVLGVKSPMQLMTFTFOVTLFTVNEFILMLLEAKDAGGSMTHTEGA 190
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 178 YFGITVAMCLPKPLREGTEBNDQRTTIPSLAMGLALFLMMFRPSVNSALIRSPIERKNA 237
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 191 YFGITVWILYRKLDOSKQROSSVYHSDLEFAMIGTIFLWITWPSFBSASPFHQDAHRA 250
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 238 VENTTYAVAVSVTAIGSSLIAPPOQKISKTYGSAVLPBGAVADTSCHLIPSPMDIVL 297
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 251 ALNTYVLSLAASVLTVTWSSIVHKKGKLDVHNIQNALAGGVGTAEMMLTPYGALIV 310
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 298 GVAAGLSVNGAKYLPCCCRNVLGIPHSISMGVPSLLGLEEIIYIVL----- 347
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 311 GFPGGISTGFAVLTFFLESRLRIQDTGGINHJGIPGIIIGVAGVTAAYSPDYGE 370
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 348 --VLDIVAGNGMIGF-----QVLISIGELSLAIVIALITGLTALLNLKIRKAPHEAKY 401
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 371 PGIVHSFGFSYKMDMKRMQGRSQIFGLLSLMAVVGIIIVGFIILKLPWQGAADENC 430
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 402 FDDOVFWK 409
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 431 FEDSIYWE 438
```

```

RESULT 7
US-10-074-978A-247
; Sequence 247, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiaohong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Faturajan, Meera
; APPLICANT: Bialock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vermet, Corine
; APPLICANT: Tcherenev, Velizar T
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Herman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A111le
; APPLICANT: Sheno, Suresh
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; TITLE OR INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269
; CURRENT APPLICATION NUMBER: US/10/074,978A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268,221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335,109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312,284
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268,496
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/276,703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330,293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322,127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280,899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 247
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Oryzoccolagus cuniculus
; US-10-074-978A-247
```

```

Query Match      22.9%; Score 486; DB 15; Length 467;
Best Local Similarity 29.1%; Pred. No. 1.4e-36;
Matches 123; Conservative 82; Mismatches 192; Indels 26; Gaps 5;
```

```

QY 13 LPLCALTLLEAALLLFFFTTHY--DA-----SLEDOKGLVAS-----YVGQDLTVM 57
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 11 LPLCLTLEAVAMVVLFLGVRYSPDADSSWSNKRKKNITSDLENEFRYRPSQDVHAM 70
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
```





APPLICANT: Burgess, Catherine E  
APPLICANT: Shimkets, Richard  
APPLICANT: Padigaru, Muralidhara  
TITLE OF INVENTION: No. US20040014081a1 Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-050 CON2  
CURRENT APPLICATION NUMBER: US/10/369, 072  
CURRENT FILING DATE: 2003-02-18  
PRIOR APPLICATION NUMBER: 10/174,372  
PRIOR FILING DATE: 2002-06-17  
PRIOR APPLICATION NUMBER: 09/898,994  
PRIOR FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: 60/215,854  
PRIOR FILING DATE: 2000-07-03  
PRIOR APPLICATION NUMBER: 60/215,856  
PRIOR FILING DATE: 2000-07-03  
PRIOR APPLICATION NUMBER: 60/215,902  
PRIOR FILING DATE: 2000-07-03  
PRIOR APPLICATION NUMBER: 60/216,585  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: 60/216,586  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: 60/216,722  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: 60/218,622  
PRIOR FILING DATE: 2000-07-17  
PRIOR APPLICATION NUMBER: 60/218,992  
PRIOR FILING DATE: 2000-07-17  
Remaining prior application data removed - See file wrapper or PALM.  
NUMBER OF SEQ ID NOS: 100  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 58  
LENGTH: 455  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-369-072-58

Query Match 22.6%; Score 480.5; DB 15; Length 455;  
Best Local Similarity 30.3%; Pred. No. 4,4e-36;  
Matches 135; Conservative 72; Mismatches 189; Indels 49; Gaps 7;  
QY 4 KYRPSVORCLPLCALTEALAILLFYFPTHY----DASL-----EDQGLVASVYGVQ 52  
DB 3 RVRHRRLVLPCLCLFGATALLFAIFVRYNHETDALMHGNSVNDNEFFRYPSFQ 62  
QY 53 DLTMAAIGGLTSSRRHSMSVAENLFMALGVQWAILLDGFLSQFPGKAVITLFS 112  
DB 63 DVHVMVFGGFLWVFLQRYGFSVSGFTFLVASLTLQWATLLQGLHSHFGHITHGVES 122  
QY 113 IWLATMSALSVLISVDVAVLQVLAQVVMVVLVEVTDLGNLRVVISNIFNTDYMNMHMI 172  
DB 123 LINAADPCAGAVLISFGAVLGKTGPAQLIMALLAVLFSVNEFTLLSLGVRDAGGSMTI 182  
QY 173 YVFAAYFGLTVAMCLPKPLPEGTEDNDORATIPSLAMTALFLMFRPVSVALLSPI 232  
DB 183 HTFGAYFGLFSLRVLRSQLEKSRHOSVYNSDLPAMIGITIFLMVFPSPNSAPFALGD 242  
QY 233 ERKKAVENTTYAAVAVSVVTAISGSSLAHPQKISKITGSHAVLPEGVAVDTSCHLISPM 292  
DB 243 GQHRTVNTYTSVLASTLSTFALSALVSGDRLDVMVQNAALAGVAVGTSSMMLTPT 302  
QY 293 LPIVLGLVAGLISVRGAKY-----LPGCC--NRVLGI PRASSINGVNFSLGLLE 340  
DB 303 GALAAGLACTAGTSLGKFFTPPILESRFKLDTCGVNINHMP-----GVLGA 350  
QY 341 IYIVLLVLDTVGA-GNGMIGFOVLLSIGELIS-----LAIYIALTSGLLTAL 386  
DB 351 ILGVVAALATHEAYGDLQGVFPLIAKGQRSAISOAVYQLFGMFTVLVFAVSGSLGGL 410  
QY 387 LTNKIKRAPHKAYPDQVFWKRP 411  
DB 411 LRLRLPDSPPDSQCFEDQVYWEVP 435

RESULT 10  
US-10-190-115-59  
Sequence 59, Application US/10190115  
Publication No. US20030207394A1  
GENERAL INFORMATION:  
APPLICANT: Alsobrook, John P. II  
APPLICANT: Boldog, Ferenc L.  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Casman, Stacie J.  
APPLICANT: Grosee, William M.  
APPLICANT: Gusev, Vladimir Y.  
APPLICANT: Ji, Weizhen  
APPLICANT: Lepley, Denise M.  
APPLICANT: Liu, Xiaohong  
APPLICANT: Merick, Amanda J.  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Patturajan, Meera  
APPLICANT: Rastelli, Luca  
APPLICANT: Shen, Lei  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Shimkets, Richard A.  
APPLICANT: Spaderna, Steven K.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Szekeres, Edward S. Jr.  
APPLICANT: Taupier, Raymond J. Jr.  
APPLICANT: Tchernev, Velizar T.  
APPLICANT: Zernhusen, Bryan D.  
APPLICANT: Voss, Edward Z.  
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: 21402-050 CIP  
CURRENT APPLICATION NUMBER: US/10/190,115  
CURRENT FILING DATE: 2003-02-10  
PRIOR APPLICATION NUMBER: 60/303,168  
PRIOR FILING DATE: 2001-07-05  
PRIOR APPLICATION NUMBER: 60/368,996  
PRIOR FILING DATE: 2002-04-01  
PRIOR APPLICATION NUMBER: 60/386,816  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: 60/215,854  
PRIOR FILING DATE: 2000-07-03  
PRIOR APPLICATION NUMBER: 60/215,856  
PRIOR FILING DATE: 2000-07-03  
PRIOR APPLICATION NUMBER: 60/216,586  
PRIOR FILING DATE: 2001-07-07  
PRIOR APPLICATION NUMBER: 60/216,722  
PRIOR FILING DATE: 2000-07-07  
PRIOR APPLICATION NUMBER: 60/218,622  
PRIOR FILING DATE: 2000-07-17  
Remaining prior application data removed - See file wrapper or PALM.  
NUMBER OF SEQ ID NOS: 136  
SOFTWARE: Curoseq1ist version 0.1  
SEQ ID NO 59  
LENGTH: 458  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-190-115-59  
Query Match 22.5%; Score 477; DB 15; Length 458;  
Best Local Similarity 29.8%; Pred. No. 9,4e-36;  
Matches 130; Conservative 75; Mismatches 203; Indels 28; Gaps 4;  
QY 4 KYRPSV---ORCLPLCALTEALAILLFYFTHYDASLE-----DQGLVASVYQ 49  
DB 3 KSPRRVAGRLPLPLCLFGATALLFAIFVRDQTDALMHGNSVNDNEFFRYRP 62  
QY 50 VQGDLTMAAIGGLTSSRRHSMSVAENLFMALGVQWAILLDGFLSQFPGKAVIT 109  
DB 63 SFQDVHVMVFGGFLWVFLQRYGFSVSGFTFLGAPALQWATLLQGLHSHFGHITHG 122

```

RESULT 11
US-10-369-072-59
; Sequence 59, Application US/10369072
Publication No. US20040014081A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John P
APPLICANT: Spaderna, Stephen K
APPLICANT: Tchernev, Velizar
APPLICANT: Liu, Xiaohong
APPLICANT: Shenoy, Suresh
APPLICANT: Spytek, Kimberly
APPLICANT: Zernusen, Bryan
APPLICANT: Patnuraajan, Meera
APPLICANT: Taupier, Raymond T
APPLICANT: Rastelli, Luca
APPLICANT: Groesse, William M
APPLICANT: Szerkeres, Edward S
APPLICANT: Lepley, Denise M
APPLICANT: Shen, Lei
APPLICANT: Burgess, Catherine E
APPLICANT: Shinkets, Richard
APPLICANT: Padiganu, Muraildhara
TITLE OF INVENTION: No. US20040014081A1e1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-050 CNS2
CURRENT APPLICATION NUMBER: US/10/369,072
PRIOR FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: 10/174,372
PRIOR FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 09/898,994
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 60/215,854
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,856
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,902
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/216,585
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,722
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/218,622
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 60/218,992
PRIOR FILING DATE: 2000-07-17
Remaining Of Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 100

```

Query Match	22.5%;	Score 477;	DB 15;	Length 458;
Best Local Similarity	29.8%;	Pred. No. 9.4e-36;		
Matches 130;	Conservative 75;	Mismatches 203;	Indels 28;	Gaps 4;

```

QY 4 KYPRSV-- -QRCLEPLCLTLEAALLILFYFPTHYDASLE-----DQKGLVASYQ 49
Db 3 KSPRVRAGRRLLPLCLCFQAGATALLFALFYRYDDOOTDAALMHGNSHNADEPFYPR 62
QY 50 VGOBLTWAAAGLIGLFTLSSFRBSWSSVAFENFMALLGVOMALLDGLSOPSPSKVIT 10
Db 63 SFQDVHVMVFPVGBEFLMVFLQRYGYSSLGFTPLLGFALQMTVLVOGFHSHFGGHVHG 127
QY 110 LFSJLWLTMSGLSVLISVDALIGKVMIAOLVVMVJVEVLDLGNLBMVISNIPTDYHNM 166
Db 123 MESJINADPCAGAVLISFCGVLIGKTPAQLLMLLALLEVALPLBNFVLLCLGRDAGS 187
QY 170 MHIVYFAAYGLVAVNACLPRLPEGEEDNDQATYPSISAMGALFLMFRPVSVALLR 223
Db 183 MTHTFPAYIGLVLKSLRYLRPHLEKSOHQSGVSHDFPAMIGTFLMI FMPSPNSALTS 244
QY 230 SPLERKNAVENTYAAVAVSVTALIGSSSLAHPOGKISITYGHSAYLPEGVAVDPSCHLR 285
Db 243 RGDGOEPYALNTYSLTASTLSLPSALNLVCKDGRGLDMVHQNALLAGVAVVGRASEMML 302
QY 290 SPMLPVLGLVGLJISVRGAKYLRGCCNRVLGIPIHSSIMGVNPSILLGLBEEIYVLLVL 349
Db 303 TPGALAAAGLGAALSTLGKFPETPLBSKLIODTCVNHAMHPGVLCALLGALMTGL 362
QY 350 DTVGA- GNGMIGFOVLSIG-----LSAIYALNTSGILLTLLNLTKIRKA 395
Db 363 TTHEAVGDDGLGVFPLIABGQRSATSQAIYOLFGLSTVLLPAGSGVGLGLKLPFLDA 422
QY 396 PHHAKTFEDVQVFWKPR 411
Db 423 PPSQCYEDQMCEVPR 438

```

```

RESULT 12
US-10-408-765A-1089
; Sequence 1089, Application US/10408765A
; Publication No. US20040101874A1
GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088,465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1089
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1089

```

Query Match	22.4%;	Score 476;	DB 16;	Length 324;
Best Local Similarity	36.1%;	Pred. No. 7.3e-36;		
Matches 112; Conservative	62;	Mismatches 124;	Indels 12;	Gaps 3;



```
/ FILE REFERENCE: 21402-050 CON2
/ CURRENT APPLICATION NUMBER: US/10/369,072
/ CURRENT FILING DATE: 2003-02-18
/ PRIOR APPLICATION NUMBER: 10/174,372
/ PRIOR FILING DATE: 2002-06-17
/ PRIOR APPLICATION NUMBER: 09/898,994
/ PRIOR FILING DATE: 2001-07-03
/ PRIOR APPLICATION NUMBER: 60/215,854
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/215,856
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/215,902
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/216,585
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 60/216,586
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 60/216,722
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 60/218,622
/ PRIOR FILING DATE: 2000-07-17
/ PRIOR APPLICATION NUMBER: 60/218,992
/ PRIOR FILING DATE: 2000-07-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 100
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 57
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Sus scrofa
/ US-10-369-072-57
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QY      62 LGFTLSFRHSSWSVAENLFMLALGVOMAILLDGFLSQPSGKVITLFSIWLATMSAL 121
DB      75 FGFMAFLQRYGFSVGFTFLAFAFLQWSTLVQGFHLTFHGHGHHGVESMINADFCAG 134
QY      122 SVLISVDVAVLGVKNLAQLVWVWVLEVTDLGNLRVYINSIFPTDYNMMNHITVFAAYFGL 181
DB      135 AVLISFGAILKGTGAQLMLLAEVULPGLNEFVLLSLGVKADAGSMTHTFGAYFGL 194
QY      182 TVAWCLPRPDEGEDNDQRTIPSLASMLGALFLMMFRPSVNSALRSPIERKNVAVNT 241
DB      195 VLSRVLYRPOLEKSKHRSQSVYHSDLFAMIGTIFLMTFWSPNSAPTRPLDQGHRTALNT 254
QY      242 YVAVAVSVVTAISGSLAHPOGKISKTYGSAVLPBGVAVDTSCHLIPSWLPIVLGLVA 301
DB      255 YSLVASTLSTFLSALVGRDGLDMVQVNAALAGVVVGTSAEMWLTFFGALAAGFLA 314
QY      302 GLISVRGAKY-----LPGCCNRVLGIPIHSSINGVNSLLGLE 339
DB      315 GTVSTLGFKEFTPTLIESKFKIOTCGVNHKGWPGVIGALLSVLVAGLATHDSYGEGLS 374
QY      340 EIIYIVLVLDTVAGNGMIGFOVLISIGELSLAIVIALTSGLLTALLNLKIRKAPHEA 399
DB      375 -----VFFLLAEGGRSSTSQLHQLFGLFTLLIFASVGGIGLLRLRPLDSPPDS 426
QY      400 KYPDQVFWKEFP 411
DB      427 QCYEDQIYWEVP 438
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RESULT 15
US-10-190-115-55
; Sequence 55, Application US/10190115
; Publication No. US20030207394A1
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/ GENERAL INFORMATION:
/ APPLICANT: Alsobrook, John P. II
/ APPLICANT: Boldog, Ferenc L.
/ APPLICANT: Burgess, Catherine E.
/ APPLICANT: Casman, Stacie J.
/ APPLICANT: Grosse, William M.
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Ji, Weizhen
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/ APPLICANT: Paturajan, Meera
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/ APPLICANT: Spaderna, Steven K.
/ APPLICANT: Spytek, Kimberly A.
/ APPLICANT: Szekeres, Edward S. Jr.
/ APPLICANT: Taupier, Raymond J. Jr.
/ APPLICANT: Tchernev, Velizar T.
/ APPLICANT: Zerhusen, Bryan D.
/ APPLICANT: Voss, Edward Z.
/ TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 21402-050 CIP
/ CURRENT APPLICATION NUMBER: US/10/190,115
/ CURRENT FILING DATE: 2003-02-10
/ PRIOR APPLICATION NUMBER: 60/303,168
/ PRIOR FILING DATE: 2001-07-05
/ PRIOR APPLICATION NUMBER: 60/368,996
/ PRIOR FILING DATE: 2002-04-01
/ PRIOR APPLICATION NUMBER: 60/386,816
/ PRIOR FILING DATE: 2002-06-07
/ PRIOR APPLICATION NUMBER: 60/215,854
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/215,856
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/215,902
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/ PRIOR APPLICATION NUMBER: 60/216,586
/ PRIOR FILING DATE: 2001-07-07
/ PRIOR APPLICATION NUMBER: 60/216,722
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 60/218,622
/ PRIOR FILING DATE: 2000-07-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 136
/ SOFTWARE: CuroSeqdist version 0.1
/ SEQ ID NO 55
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-190-115-55

Query Match      22.0%; Score 466.5; DB 15; Length 458;
Best Local Similarity 29.5%; Pred. No. 9e-35;
Matches 125; Conservative 78; Mismatches 196; Indels 25; Gaps 4;

QY      13 LPLCALTEALAILLFYFTTHY-----DASLEDQK-----LVASVYGODLTWMAIG 61
DB      15 LPLCLFLQAGATVAVLFAVFRVYNNHTDALMHRNSHNSNADNFYFRYPSQDVHTMTFVG 74
QY      62 LGFTLSFRHSSWSVAENLFMLALGVOMAILLDGFLSQPSGKVITLFSIWLATMSAL 121
DB      75 FGFMAFLQRYGFSVGFTFLAFAFLQWSTLVQGFHLTFHGHGHHGVESMINADFCAG 134
QY      122 SVLISVDVAVLGVKNLAQLVWVWVLEVTDLGNLRVYINSIFPTDYNMMNHITVFAAYFGL 181
DB      135 AVLISFGAVLKGTPQQLMLLAEVULPGLNEFVLLHLSGRVADAGSMTHTFGAYFGL 194
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